

SEQUENCE LISTING

<110> Guarente, Leonard P.
 Austriaco Jr., Nicanor
 Claus, James J.
 Cole, Francesca
 Kennedy, Brian

<120> GENES DETERMINING CELLULAR SENESCENCE IN
 YEAST

<130> 0050.1491-005

<150> US 08/396,001
<151> 1995-02-28

<150> PCT/US94/09351
<151> 1994-08-15

<150> US 08/107,408
<151> 1993-08-16

<150> US 09/323,433
<151> 1999-06-01

<160> 48

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1946
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (322)...(1671)
<223> UTH1

<400> 1
tgaaaaagtg gaactagacc ccacgtcagc gggccttaggc cttcaatgt gttagaatac 60
acagcggtcc tagttcttgg tgctggatc tcgaggccgc ggacttgaa aagcccttcc 120
ttttccagat cgggaaacct aatgagtcca taaaaagaaaa tgttagaggtg gtgttgacgt 180
tttgcgcgtt ttgggcaagt aggtcttct gcacggccccg gcccgggtcg tgcggaaaaaa 240
gaaaaaaagca gacaaaaacaa aatttttcct tttttcgcct tttgtttctc ctgattcggg 300
tatataagtg aataccatct a atg tgt ttc ctt ctc gag acc tcg gcg tct 351
Met Cys Phe Leu Leu Glu Thr Ser Ala Ser
1 5 10

ccc aga tca aag ctc agc aaa gat ttt aaa ccg caa ttt acg ctc ctt 399
Pro Arg Ser Lys Leu Ser Lys Asp Phe Lys Pro Gln Phe Thr Leu Leu
15 20 25

tca tcg gta act aag aag aaa aaa aaa gta cga cca cac aat ttc 447
Ser Ser Val Thr Lys Lys Lys Lys Lys Val Arg Pro His Asn Phe
30 35 40

cag tgt att cat tcc tta aac ttc gtt tat ttt tta ttc att cat tca Gln Cys Ile His Ser Leu Asn Phe Val Tyr Phe Leu Phe Ile His Ser	45	50	55	495
ttt tta ttt gaa tat aac caa cta cta gtc ctt cct tta aac aaa aat Phe Leu Phe Glu Tyr Asn Gln Leu Leu Val Leu Pro Leu Asn Lys Asn	60	65	70	543
tta ccc tcc ctt aat ttt tca aga aat tcc agt atg aaa tta tcc gct Leu Pro Ser Leu Asn Phe Ser Arg Asn Ser Met Lys Leu Ser Ala	75	80	85	591
ctc tta gct tta tca gcc tcc acc gcc gtc ttg gcc gct cca gct gtc Leu Leu Ala Leu Ser Ala Ser Thr Ala Val Leu Ala Ala Pro Ala Val	95	100	105	639
cac cat agt gac aac cac cac aac gac aag cgt gcc gtt gtc acc His His Ser Asp Asn His His Asn Asp Lys Arg Ala Val Val Thr	110	115	120	687
gtt act cag tac gtc aac gca gac ggc gct gtt gtt att cca gct gcc Val Thr Gln Tyr Val Asn Ala Asp Gly Ala Val Val Ile Pro Ala Ala	125	130	135	735
acc acc gct acc tcg gcg gct gct gat gga aag gtc gag tct gtt gct Thr Thr Ala Ala Ser Ala Asp Gly Lys Val Glu Ser Val Ala	140	145	150	783
gct gcc acc act act ttg tcc tcg act gcc gcc gct act acc tct Ala Ala Thr Thr Leu Ser Ser Thr Ala Ala Ala Thr Thr Ser	155	160	165	831
gcc gcc gcc tct tct tcc tcc tct tcc tcc tct tcc tct tcc tct Ala Ala Ala Ser	175	180	185	879
tcc tct gtt ggt tct gga gat ttt gaa gat ggt acc att tcc tgt tct Ser Ser Val Gly Ser Gly Asp Phe Glu Asp Gly Thr Ile Ser Cys Ser	190	195	200	927
gat ttc cca tcc gga caa ggt gct gtc tcc ttg gac tgg tta ggt cta Asp Phe Pro Ser Gly Gln Gly Ala Val Ser Leu Asp Trp Leu Gly Leu	205	210	215	975
ggc ggc tgg gct tcc atc atg gac atg aac ggt aac acc gcc acc tct Gly Gly Trp Ala Ser Ile Met Asp Met Asn Gly Asn Thr Ala Thr Ser	220	225	230	1023
tgt caa gac gga tac tac tgt tct tac gct tgt tct cca ggt tac gct Cys Gln Asp Gly Tyr Tyr Cys Ser Tyr Ala Cys Ser Pro Gly Tyr Ala	235	240	245	1071
aag acc caa tgg cct tct gaa caa cct tcc gat ggt aga tcc gtt ggt Lys Thr Gln Trp Pro Ser Glu Gln Pro Ser Asp Gly Arg Ser Val Gly	255	260	265	1119
ggc tta tac tgt aag aac ggt aaa tta tac cgt tcc aac acc gac act Gly Leu Tyr Cys Lys Asn Gly Lys Leu Tyr Arg Ser Asn Thr Asp Thr	270	275	280	1167

aac agt ttg tgt gta gaa ggt caa ggc tct gct caa gct gtt aac aag Asn Ser Leu Cys Val Glu Gly Gln Gly Ser Ala Gln Ala Val Asn Lys 285 290 295	1215
gtc tcc ggc tcc att gct atc tgt ggt acc gat tat cca ggt tct gaa Val Ser Gly Ser Ile Ala Ile Cys Gly Thr Asp Tyr Pro Gly Ser Glu 300 305 310	1263
aac atg gtc gtt cct acc gta gtt ggc gct ggt tcc tcc caa cca atc Asn Met Val Val Pro Thr Val Val Gly Ala Gly Ser Ser Gln Pro Ile 315 320 325 330	1311
aac gtc atc aag gag gac tcc tac tat caa tgg caa ggt aag aag acc Asn Val Ile Lys Glu Asp Ser Tyr Tyr Gln Trp Gln Gly Lys Lys Thr 335 340 345	1359
tct gcc caa tac tac gtt aac aac gct ggt gtc tct gtg gaa gat ggt Ser Ala Gln Tyr Tyr Val Asn Asn Ala Gly Val Ser Val Glu Asp Gly 350 355 360	1407
tgt atc tgg ggt act gag ggt tcc ggt gtc ggt aac tgg gcc cca gtt Cys Ile Trp Gly Thr Glu Gly Ser Gly Val Gly Asn Trp Ala Pro Val 365 370 375	1455
gtc ttg ggt gct ggt tac act gat ggt atc act tac ttg tcc atc att Val Leu Gly Ala Gly Tyr Thr Asp Gly Ile Thr Tyr Leu Ser Ile Ile 380 385 390	1503
cca aac cca aac aac aaa gaa gca cca aac ttt aac atc aag atc gtt Pro Asn Pro Asn Asn Lys Glu Ala Pro Asn Phe Asn Ile Lys Ile Val 395 400 405 410	1551
gcc acc gat ggc tct acc gtc aat ggt gct tgc tct tac gaa aat ggt Ala Thr Asp Gly Ser Thr Val Asn Gly Ala Cys Ser Tyr Glu Asn Gly 415 420 425	1599
gtc tac tct ggc tct ggc tct gac ggt tgt act gtt tca gtt act tct Val Tyr Ser Gly Ser Asp Gly Cys Thr Val Ser Val Thr Ser 430 435 440	1647
ggg tct gct aac ttt gtc ttc tac taggcctttt ttccttgaat attgcaaata Gly Ser Ala Asn Phe Val Phe Tyr 445 450	1701
agcttttgct agtacttttt ttactccgtt cattttatgg tttattttc aatttagttcg ttttccaca atacaaaaaa acacagtccct ttgtactatc ccttttattt cattatttt tctttttaa gataccacta gatattatca tatatacat attatataac ataaaaagtc aagaaaaaaa atgttttat cacttctat aactgcatac cttttttgc atttcgaatg attgc	1761 1821 1881 1941 1946
<210> 2	
<211> 450	
<212> PRT	
<213> Saccharomyces cerevisiae	
<220>	
<221> VARIANT	
<222> (1)...(441)	

<223> Xaa = Any Amino Acid

<400> 2
 Met Cys Phe Leu Leu Glu Thr Ser Ala Ser Pro Arg Ser Lys Leu Ser
 1 5 10 15
 Lys Asp Phe Lys Pro Gln Phe Thr Leu Leu Ser Ser Val Thr Lys Lys
 20 25 30
 Lys Lys Lys Val Arg Pro His Asn Phe Gln Cys Ile His Ser Leu
 35 40 45
 Asn Phe Val Tyr Phe Leu Phe Ile His Ser Phe Leu Phe Glu Tyr Asn
 50 55 60
 Gln Leu Leu Val Leu Pro Leu Asn Lys Asn Leu Pro Ser Leu Asn Phe
 65 70 75 80
 Ser Arg Asn Ser Ser Met Lys Leu Ser Ala Leu Leu Ala Leu Ser Ala
 85 90 95
 Ser Thr Ala Val Leu Ala Ala Pro Ala Val His His Ser Asp Asn His
 100 105 110
 His His Asn Asp Lys Arg Ala Val Val Thr Val Thr Gln Tyr Val Asn
 115 120 125
 Ala Asp Gly Ala Val Val Ile Pro Ala Ala Thr Thr Ala Thr Ser Ala
 130 135 140
 Ala Ala Asp Gly Lys Val Glu Ser Val Ala Ala Thr Thr Thr Leu
 145 150 155 160
 Ser Ser Thr Ala Ala Ala Ala Thr Thr Ser Ala Ala Ala Ser Ser Ser
 165 170 175
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Val Gly Ser Gly
 180 185 190
 Asp Phe Glu Asp Gly Thr Ile Ser Cys Ser Asp Phe Pro Ser Gly Gln
 195 200 205
 Gly Ala Val Ser Leu Asp Trp Leu Gly Leu Gly Trp Ala Ser Ile
 210 215 220
 Met Asp Met Asn Gly Asn Thr Ala Thr Ser Cys Gln Asp Gly Tyr Tyr
 225 230 235 240
 Cys Ser Tyr Ala Cys Ser Pro Gly Tyr Ala Lys Thr Gln Trp Pro Ser
 245 250 255
 Glu Gln Pro Ser Asp Gly Arg Ser Val Gly Gly Leu Tyr Cys Lys Asn
 260 265 270
 Gly Lys Leu Tyr Arg Ser Asn Thr Asp Thr Asn Ser Leu Cys Val Glu
 275 280 285
 Gly Gln Gly Ser Ala Gln Ala Val Asn Lys Val Ser Gly Ser Ile Ala
 290 295 300
 Ile Cys Gly Thr Asp Tyr Pro Gly Ser Glu Asn Met Val Val Pro Thr
 305 310 315 320
 Val Val Gly Ala Gly Ser Ser Gln Pro Ile Asn Val Ile Lys Glu Asp
 325 330 335
 Ser Tyr Tyr Trp Gln Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Val
 340 345 350
 Asn Asn Ala Gly Val Ser Val Glu Asp Gly Cys Ile Trp Gly Thr Glu
 355 360 365
 Gly Ser Gly Val Gly Asn Trp Ala Pro Val Val Leu Gly Ala Gly Tyr
 370 375 380
 Thr Asp Gly Ile Thr Tyr Leu Ser Ile Ile Pro Asn Pro Asn Asn Lys
 385 390 395 400
 Glu Ala Pro Asn Phe Asn Ile Lys Ile Val Ala Thr Asp Gly Ser Thr
 405 410 415
 Val Asn Gly Ala Cys Ser Tyr Glu Asn Gly Val Tyr Ser Gly Ser Gly
 420 425 430
 Ser Asp Gly Cys Thr Val Ser Val Thr Ser Gly Ser Ala Asn Phe Val
 435 440 445

Phe Tyr
450

<210> 3
<211> 3455
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (663) ... (3164)
<223> UTH4

<400> 3
aagctttaac gggatcttct aacaacaaat agcataataa ccaaaaacca gtttcagtgg 60
gatcagccct a tcgacacgccc ttttttagcg gtcttaacaat ctccgtttat gtcgtatgg 120
atttctatac ttgaccctac cttatttctc gaatatgcct ataaggattt tctcgaaaga 180
agggcttcgg gaaagaggcg cctcaggccaa aaatgagcaa aaaaaaaaaaaa aaaaagaaaa 240
gattcgaaga tctatgaaaa atttatgcag attcgttgag agtataagg attttactct 300
ttatgggtat agggttcatt ctaaaatcaa gcataaaat ttgtgtttgt ctccctcttt 360
tcctgtcctc ttttttgcc atcctctgtc gccattgaag tcgaacttta tagatagatt 420
tactcttgcatt tctcacgcatt ctcaggccac ctggacactg tacatggttg tgattgttct 480
ctttctcagt tatcgaatatttgcatt ttatactcca aaatcggctc tgcacacgccc 540
ttatttttgt ggtttcaatt tactaacaca acattctttt attcaatcag atcaataacg 600
aaccattttcc atctgccgac tcagcatcga ttttaactac gtctacatca aataactcct 660
ta atg tct tac aat cat cag cct caa cta tct att aac tcc gtc caa 707

Met Ser Tyr Asn His Gln Pro Gln Leu Ser Ile Asn Ser Val Gln
1 5 10 15

tca ctc ttg gag ccc gtg acc cct ccg cct ttg ggc cag atg aat aac 755
Ser Leu Leu Glu Pro Val Thr Pro Pro Leu Gly Gln Met Asn Asn
20 25 30

aaa aga aac cat caa aag gct cat tcg ctt gat ctc tct ggt ttt aat 803
Lys Arg Asn His Gln Lys Ala His Ser Leu Asp Leu Ser Gly Phe Asn
35 40 45

cag ttc ata tca tcg aca caa tct ccc ttg gct ttg atg aat aat aca 851
Gln Phe Ile Ser Ser Thr Gln Ser Pro Leu Ala Leu Met Asn Asn Thr
50 55 60

tca aca tcg aat tct gct aac tct ttt tcc ccg aat cct aat gct gct 899
Ser Thr Ser Asn Ser Ala Asn Ser Phe Ser Pro Asn Pro Asn Ala Ala
65 70 75

agc aac tcc act ggg ctt tca gcc tca atg gca aat cct cca gcc att 947
Ser Asn Ser Thr Gly Leu Ser Ala Ser Met Ala Asn Pro Pro Ala Ile
80 85 90 95

cta cca tta atc aat gag ttt gat ctg gaa atg gat ggt ccc agg aga 995
Leu Pro Leu Ile Asn Glu Phe Asp Leu Glu Met Asp Gly Pro Arg Arg
100 105 110

aaa tca agc cac gat ttc acg gtt gtt gct cct tcg aac tct ggt gtc 1043
Lys Ser Ser His Asp Phe Thr Val Val Ala Pro Ser Asn Ser Gly Val
115 120 125

aat acc tcc agt tta att atg gaa aca cca tcc tct tca gtg act cct 1091

Asn Thr Ser Ser Leu Ile Met Glu Thr Pro Ser Ser Ser Val Thr Pro			
130	135	140	
gct gca tct ctc aga aat ttt agc aat agt aat aat gct gct tcc aaa			1139
Ala Ala Ser Leu Arg Asn Phe Ser Asn Ser Asn Ala Ala Ser Lys			
145	150	155	
tgt gga gtg gat aat tcg tca ttt ggt ttg agt agc tca acg tct tca			1187
Cys Gly Val Asp Asn Ser Ser Phe Gly Leu Ser Ser Ser Thr Ser Ser			
160	165	170	175
tct atg gtc gaa atc agc gca cta ccc ctt aga gat ctg gat tat atc			1235
Ser Met Val Glu Ile Ser Ala Leu Pro Leu Arg Asp Leu Asp Tyr Ile			
180	185	190	
aaa ctt gcc act gac cag ttt ggc tgc cgt ttt ctt caa aaa aaa tta			1283
Lys Leu Ala Thr Asp Gln Phe Gly Cys Arg Phe Leu Gln Lys Lys Leu			
195	200	205	
gaa acc ccc agt gaa tcc aat atg gtg aga gac ttg atg tat gaa caa			1331
Glu Thr Pro Ser Glu Ser Asn Met Val Arg Asp Leu Met Tyr Glu Gln			
210	215	220	
att aag cca ttt ttc ttg gac ctt att ttg gat ccg ttc ggt aac tat			1379
Ile Lys Pro Phe Phe Leu Asp Leu Ile Leu Asp Pro Phe Gly Asn Tyr			
225	230	235	
ttg gtt caa aaa cta tgc gat tat tta act gcc gag caa aag aca tta			1427
Leu Val Gln Lys Leu Cys Asp Tyr Leu Thr Ala Glu Gln Lys Thr Leu			
240	245	250	255
tta ata caa aca ata tat cca aat gtt ttc caa ata tca atc aat cag			1475
Leu Ile Gln Thr Ile Tyr Pro Asn Val Phe Gln Ile Ser Ile Asn Gln			
260	265	270	
tac gga act cgt tcc tta cag aaa att ata gac act gtc gat aac gaa			1523
Tyr Gly Thr Arg Ser Leu Gln Lys Ile Ile Asp Thr Val Asp Asn Glu			
275	280	285	
gtt caa atc gat ctc att att aag gga ttt tcc caa gaa ttt act tcg			1571
Val Gln Ile Asp Leu Ile Ile Lys Gly Phe Ser Gln Glu Phe Thr Ser			
290	295	300	
att gag caa gtg gtt act ttg ata aac gat ctt aat ggt aac cat gtg			1619
Ile Glu Gln Val Val Thr Leu Ile Asn Asp Leu Asn Gly Asn His Val			
305	310	315	
att caa aag tgt att ttc aaa ttc tcg cca tca aaa ttt ggt ttc atc			1667
Ile Gln Lys Cys Ile Phe Lys Phe Ser Pro Ser Lys Phe Gly Phe Ile			
320	325	330	335
ata gat gct att gta gaa caa aat aat atc att acc att tct acc cat			1715
Ile Asp Ala Ile Val Glu Gln Asn Asn Ile Ile Thr Ile Ser Thr His			
340	345	350	
aaa cat ggt tgt tgc gta cta caa aaa tta cta agc gtt tgt act cta			1763
Lys His Gly Cys Cys Val Leu Gln Lys Leu Leu Ser Val Cys Thr Leu			
355	360	365	

caa caa att ttc aaa att tct gtg aaa att gtg cag ttc ctt cct gga Gln Gln Ile Phe Lys Ile Ser Val Lys Ile Val Gln Phe Leu Pro Gly 370 375 380	1811
tta atc aac gat cag ttc ggt aat tat atc atc caa ttt ctg tta gat Leu Ile Asn Asp Gln Phe Gly Asn Tyr Ile Ile Gln Phe Leu Leu Asp 385 390 395	1859
atc aaa gaa ttg gac ttt tac tta ttg gct gag tta ttt aac cgt tta Ile Lys Glu Leu Asp Phe Tyr Leu Leu Ala Glu Leu Phe Asn Arg Leu 400 405 410 415	1907
tcc aat gaa tta tgt caa cta tct tgt ttg aag ttc tcc tca aat gtt Ser Asn Glu Leu Cys Gln Leu Ser Cys Leu Lys Phe Ser Ser Asn Val 420 425 430	1955
gtg gaa aaa ttc att aaa aaa tta ttt aga atc att act gga ttt att Val Glu Lys Phe Ile Lys Leu Phe Arg Ile Ile Thr Gly Phe Ile 435 440 445	2003
gtt aat aac aat ggg ggt gcc tcc caa agg act gca gtt gct tct gat Val Asn Asn Asn Gly Gly Ala Ser Gln Arg Thr Ala Val Ala Ser Asp 450 455 460	2051
gac gtg att aat gct tct atg aac att ctt ttg act acc att gat ata Asp Val Ile Asn Ala Ser Met Asn Ile Leu Leu Thr Thr Ile Asp Ile 465 470 475	2099
ttc aca gtc aat tta aat gtg cta atc agg gat aat ttt ggt aat tat Phe Thr Val Asn Leu Asn Val Leu Ile Arg Asp Asn Phe Gly Asn Tyr 480 485 490 495	2147
gcg tta caa acg cta tta gac gtt aag aat tat tct cct ctg ctt gct Ala Leu Gln Thr Leu Leu Asp Val Lys Asn Tyr Ser Pro Leu Leu Ala 500 505 510	2195
tac aac aaa aat agt aac gca att ggg caa aac agc tct agt aca ttg Tyr Asn Lys Asn Ser Asn Ala Ile Gly Gln Asn Ser Ser Thr Leu 515 520 525	2243
aat tac ggt aac ttt tgt aac gat ttt tca ttg aaa att ggt aac ttg Asn Tyr Asn Phe Cys Asn Asp Phe Ser Leu Lys Ile Gly Asn Leu 530 535 540	2291
att gtc ctt aca aaa gaa tta ctt cca agt att aaa act aca tcc tat Ile Val Leu Thr Lys Glu Leu Leu Pro Ser Ile Lys Thr Thr Ser Tyr 545 550 555	2339
gca aag aaa att aag ttg aaa gtt aaa gct tat gca gaa gcc aca ggt Ala Lys Lys Ile Lys Leu Lys Val Lys Ala Tyr Ala Glu Ala Thr Gly 560 565 570 575	2387
ata cca ttc act gac ata tct cct caa gtc act gca atg agt cat aac Ile Pro Phe Thr Asp Ile Ser Pro Gln Val Thr Ala Met Ser His Asn 580 585 590	2435
aat ctt caa acg att aac aac gaa aat aag aac ccc cat aac aaa aat Asn Leu Gln Thr Ile Asn Asn Glu Asn Lys Asn Pro His Asn Lys Asn 595 600 605	2483

agt cat aat cat aat cat aat cat aat cat aac cat gct cac aat aat Ser His Asn His His His His His His His Ala His His Asn Asn 610 615 620	2531
aat aac aat aat aat caa aag agt cat acc cgt cat ttt tct tta cca Asn Asn Asn Asn Gln Lys Ser His Thr Arg His Phe Ser Leu Pro 625 630 635	2579
gct aat gct tac cat aga aga agt aac agc tct gta acc aat aat ttc Ala Asn Ala Tyr His Arg Arg Ser Asn Ser Val Thr Asn Asn Phe 640 645 650 655	2627
tca aac caa tat gca caa gat cag aaa att cac tct ccg caa caa att Ser Asn Gln Tyr Ala Gln Asp Gln Lys Ile His Ser Pro Gln Gln Ile 660 665 670	2675
atg aac ttc aac caa aac gca tat ccc tcg atg gga gca cct tct ttc Met Asn Phe Asn Gln Asn Ala Tyr Pro Ser Met Gly Ala Pro Ser Phe 675 680 685	2723
aat tct caa act aac cca cca ttg gta agc cat aac tcg tta caa aac Asn Ser Gln Thr Asn Pro Pro Leu Val Ser His Asn Ser Leu Gln Asn 690 695 700	2771
ttc gac aac cgc cag ttt gca aat tta atg gca cat cct aat tct gct Phe Asn Arg Gln Phe Ala Asn Leu Met Ala His Pro Asn Ser Ala 705 710 715	2819
gca cca atc cat tcg ttc tca tca tct aac att acc aat gtg aat cct Ala Pro Ile His Ser Phe Ser Ser Asn Ile Thr Asn Val Asn Pro 720 725 730 735	2867
aat gtt tca agg gga ttt aag cag cct gga ttt atg atg aat gaa acc Asn Val Ser Arg Gly Phe Lys Gln Pro Gly Phe Met Met Asn Glu Thr 740 745 750	2915
gac aaa att aat gct aat cac ttc tcg cca tac tct aat gca aat agt Asp Lys Ile Asn Ala Asn His Phe Ser Pro Tyr Ser Asn Ala Asn Ser 755 760 765	2963
caa aac ttc aat gaa tct ttt gtg cct cgt atg caa tat caa acg gaa Gln Asn Phe Asn Glu Ser Phe Val Pro Arg Met Gln Tyr Gln Thr Glu 770 775 780	3011
ggg gca aac tgg gat tca agt ttg tca atg aag tcg cag cat att ggt Gly Ala Asn Trp Asp Ser Ser Leu Ser Met Lys Ser Gln His Ile Gly 785 790 795	3059
caa ggc cca tat aat caa gtt aat atg agc cgc aac gct agt att tcc Gln Gly Pro Tyr Asn Gln Val Asn Met Ser Arg Asn Ala Ser Ile Ser 800 805 810 815	3107
aat atg cct gcc atg aat acc gct aga aca tct gat gaa ctt caa ttc Asn Met Pro Ala Met Asn Thr Ala Arg Thr Ser Asp Glu Leu Gln Phe 820 825 830	3155
act ttg cca taatactttt ttttctttct ttttctttcc ttcttactgt Thr Leu Pro	3204

acaaatattt tacgcagaaa tcaaagacaa aagaaaaata aaaaataaaaa aataaaaaat 3264
 tcaactaaggc aatgacgtcc tactaaagtgc cccaaaatttg agccggaaaa aaatggtaaa 3324
 gcaaaactattt gccatctta tattttgtat tctgtttccg aacacgtatc caaaaatcctc 3384
 ccactgcctt tgccagggtta gcattgctcc ctacccaaat gatctaattt tttttgaat 3444
 cgttttttgtt c 3455

<210> 4
 <211> 834
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 4
 Met Ser Tyr Asn His Gln Pro Gln Leu Ser Ile Asn Ser Val Gln Ser
 1 5 10 15
 Leu Leu Glu Pro Val Thr Pro Pro Leu Gly Gln Met Asn Asn Lys
 20 25 30
 Arg Asn His Gln Lys Ala His Ser Leu Asp Leu Ser Gly Phe Asn Gln
 35 40 45
 Phe Ile Ser Ser Thr Gln Ser Pro Leu Ala Leu Met Asn Asn Thr Ser
 50 55 60
 Thr Ser Asn Ser Ala Asn Ser Phe Ser Pro Asn Pro Asn Ala Ala Ser
 65 70 75 80
 Asn Ser Thr Gly Leu Ser Ala Ser Met Ala Asn Pro Pro Ala Ile Leu
 85 90 95
 Pro Leu Ile Asn Glu Phe Asp Leu Glu Met Asp Gly Pro Arg Arg Lys
 100 105 110
 Ser Ser His Asp Phe Thr Val Val Ala Pro Ser Asn Ser Gly Val Asn
 115 120 125
 Thr Ser Ser Leu Ile Met Glu Thr Pro Ser Ser Val Thr Pro Ala
 130 135 140
 Ala Ser Leu Arg Asn Phe Ser Asn Ser Asn Asn Ala Ala Ser Lys Cys
 145 150 155 160
 Gly Val Asp Asn Ser Ser Phe Gly Leu Ser Ser Ser Thr Ser Ser
 165 170 175
 Met Val Glu Ile Ser Ala Leu Pro Leu Arg Asp Leu Asp Tyr Ile Lys
 180 185 190
 Leu Ala Thr Asp Gln Phe Gly Cys Arg Phe Leu Gln Lys Lys Leu Glu
 195 200 205
 Thr Pro Ser Glu Ser Asn Met Val Arg Asp Leu Met Tyr Glu Gln Ile
 210 215 220
 Lys Pro Phe Phe Leu Asp Leu Ile Leu Asp Pro Phe Gly Asn Tyr Leu
 225 230 235 240
 Val Gln Lys Leu Cys Asp Tyr Leu Thr Ala Glu Gln Lys Thr Leu Leu
 245 250 255
 Ile Gln Thr Ile Tyr Pro Asn Val Phe Gln Ile Ser Ile Asn Gln Tyr
 260 265 270
 Gly Thr Arg Ser Leu Gln Lys Ile Ile Asp Thr Val Asp Asn Glu Val
 275 280 285
 Gln Ile Asp Leu Ile Ile Lys Gly Phe Ser Gln Glu Phe Thr Ser Ile
 290 295 300
 Glu Gln Val Val Thr Leu Ile Asn Asp Leu Asn Gly Asn His Val Ile
 305 310 315 320
 Gln Lys Cys Ile Phe Lys Phe Ser Pro Ser Lys Phe Gly Phe Ile Ile
 325 330 335
 Asp Ala Ile Val Glu Gln Asn Asn Ile Ile Thr Ile Ser Thr His Lys
 340 345 350
 His Gly Cys Cys Val Leu Gln Lys Leu Leu Ser Val Cys Thr Leu Gln
 355 360 365

Gln Ile Phe Lys Ile Ser Val Lys Ile Val Gln Phe Leu Pro Gly Leu
 370 375 380
 Ile Asn Asp Gln Phe Gly Asn Tyr Ile Ile Gln Phe Leu Leu Asp Ile
 385 390 395 400
 Lys Glu Leu Asp Phe Tyr Leu Leu Ala Glu Leu Phe Asn Arg Leu Ser
 405 410 415
 Asn Glu Leu Cys Gln Leu Ser Cys Leu Lys Phe Ser Ser Asn Val Val
 420 425 430
 Glu Lys Phe Ile Lys Lys Leu Phe Arg Ile Ile Thr Gly Phe Ile Val
 435 440 445
 Asn Asn Asn Gly Gly Ala Ser Gln Arg Thr Ala Val Ala Ser Asp Asp
 450 455 460
 Val Ile Asn Ala Ser Met Asn Ile Leu Leu Thr Thr Ile Asp Ile Phe
 465 470 475 480
 Thr Val Asn Leu Asn Val Leu Ile Arg Asp Asn Phe Gly Asn Tyr Ala
 485 490 495
 Leu Gln Thr Leu Leu Asp Val Lys Asn Tyr Ser Pro Leu Leu Ala Tyr
 500 505 510
 Asn Lys Asn Ser Asn Ala Ile Gly Gln Asn Ser Ser Ser Thr Leu Asn
 515 520 525
 Tyr Gly Asn Phe Cys Asn Asp Phe Ser Leu Lys Ile Gly Asn Leu Ile
 530 535 540
 Val Leu Thr Lys Glu Leu Leu Pro Ser Ile Lys Thr Thr Ser Tyr Ala
 545 550 555 560
 Lys Lys Ile Lys Leu Lys Val Lys Ala Tyr Ala Glu Ala Thr Gly Ile
 565 570 575
 Pro Phe Thr Asp Ile Ser Pro Gln Val Thr Ala Met Ser His Asn Asn
 580 585 590
 Leu Gln Thr Ile Asn Asn Glu Asn Lys Asn Pro His Asn Lys Asn Ser
 595 600 605
 His Asn His Asn His Asn His Asn His Asn His Asn Asn Asn
 610 615 620
 Asn Asn Asn Asn Gln Lys Ser His Thr Arg His Phe Ser Leu Pro Ala
 625 630 635 640
 Asn Ala Tyr His Arg Arg Ser Asn Ser Ser Val Thr Asn Asn Phe Ser
 645 650 655
 Asn Gln Tyr Ala Gln Asp Gln Lys Ile His Ser Pro Gln Gln Ile Met
 660 665 670
 Asn Phe Asn Gln Asn Ala Tyr Pro Ser Met Gly Ala Pro Ser Phe Asn
 675 680 685
 Ser Gln Thr Asn Pro Pro Leu Val Ser His Asn Ser Leu Gln Asn Phe
 690 695 700
 Asp Asn Arg Gln Phe Ala Asn Leu Met Ala His Pro Asn Ser Ala Ala
 705 710 715 720
 Pro Ile His Ser Phe Ser Ser Ser Asn Ile Thr Asn Val Asn Pro Asn
 725 730 735
 Val Ser Arg Gly Phe Lys Gln Pro Gly Phe Met Met Asn Glu Thr Asp
 740 745 750
 Lys Ile Asn Ala Asn His Phe Ser Pro Tyr Ser Asn Ala Asn Ser Gln
 755 760 765
 Asn Phe Asn Glu Ser Phe Val Pro Arg Met Gln Tyr Gln Thr Glu Gly
 770 775 780
 Ala Asn Trp Asp Ser Ser Leu Ser Met Lys Ser Gln His Ile Gly Gln
 785 790 795 800
 Gly Pro Tyr Asn Gln Val Asn Met Ser Arg Asn Ala Ser Ile Ser Asn
 805 810 815
 Met Pro Ala Met Asn Thr Ala Arg Thr Ser Asp Glu Leu Gln Phe Thr
 820 825 830
 Leu Pro

<210> 5
<211> 4000
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (717) ... (3380)
<223> YGL023

<400> 5
gtgtcttcca tggagtgaat tggattttgtt gaatttatatac tggccaaatac cgttgccttg 60
ttggagctc agatagaaaa gacatcttaa ttccagacag tctattctct gtctatttct 120
ctttgtact gcaaaatttaa atttgtgacg cttttctta ttactcatgt atttgtca 180
cttgacgatt gtttttttc tatattttt ttgttctggg gtctccaga gaataaaaaa 240
taatgatcaa tataatgtat agtataatgttta tattcttatt cgttgcaccc tttttacaa 300
atcacatcaga ctcaaaagaga atatcggttg gttatcttc tccgaagggtg aacagcaaac 360
agtagctcac gtctttttt tgaatagttt tttttttgt tgaaacagaa aaaaaacttt 420
cttccgtata ttacattgtt cattattttt attgtatattt agtttccaac gttaggattt 480
gagccgtcat taatattttt cgttttgtt cactatttca gacgattttt ttttagtaca 540
cttaaaaattt cttgttgatat tggccacttag ttctcttttcc atatttttt ttcgcttattt 600
ctttaggttc tttaaagagt ctctgttcat ttccgttct tactgtttct ttgtcctcga 660
tatcttttaa gaaagagaga actaagcgct gtaacatttt taagtggacc tacgtt atg 719
Met
1
tct aca aaa ggt ttg aaa gaa gaa atc gat gat gta cca tca gta gac 767
Ser Thr Lys Gly Leu Lys Glu Glu Ile Asp Asp Val Pro Ser Val Asp
5 10 15
cct gtc gtt tca gaa aca gtc aat tct gct tta gag cag ttg caa cta 815
Pro Val Val Ser Glu Thr Val Asn Ser Ala Leu Glu Gln Leu Gln Leu
20 25 30
gat gat cca gag gaa aac gcc acc tct aat gca ttt gcg aat aaa gtt 863
Asp Asp Pro Glu Glu Asn Ala Thr Ser Asn Ala Phe Ala Asn Lys Val
35 40 45
tct caa gat tct caa ttc gct aat ggc cct ccg tcg caa atg ttt cca 911
Ser Gln Asp Ser Gln Phe Ala Asn Gly Pro Pro Ser Gln Met Phe Pro
50 55 60 65
cat cca caa atg atg ggt gga atg ggc ttc atg ccc tac tct caa atg 959
His Pro Gln Met Met Gly Gly Met Gly Phe Met Pro Tyr Ser Gln Met
70 75 80
atg cag gtt cct cat aat cct tgt cca ttt ttt ccg ccc cct gat ttt 1007
Met Gln Val Pro His Asn Pro Cys Pro Phe Phe Pro Pro Asp Phe
85 90 95
aat gat cca aca gca cca ttg agt agc tcg ccc ttg aat gca ggc ggt 1055
Asn Asp Pro Thr Ala Pro Leu Ser Ser Pro Leu Asn Ala Gly Gly
100 105 110
cca cca atg tta ttc aag aat gac tca ctt cca ttt caa atg ctg tct 1103

Pro Pro Met Leu Phe Lys Asn Asp Ser Leu Pro Phe Gln Met Leu Ser			
115	120	125	
tcg ggt gct gcg gta gca actcaa ggt gga caaa atctaa cta aacccat ttg			1151
Ser Gly Ala Ala Val Ala Thr Gln Gly Gly Gln Asn Leu Asn Pro Leu			
130	135	140	145
ata aat gac aat tca atg aag gta ttg cca atc gca tcg gct gat ccg			1199
Ile Asn Asp Asn Ser Met Lys Val Leu Pro Ile Ala Ser Ala Asp Pro			
150	155	160	
tta tgg act cat tca aac gta cca gga tca gca tct gta gcc att gaa			1247
Leu Trp Thr His Ser Asn Val Pro Gly Ser Ala Ser Val Ala Ile Glu			
165	170	175	
gaa acc acc gct act cta caa gaa agc cta cca tct aag ggc agg gag			1295
Glu Thr Thr Ala Thr Leu Gln Glu Ser Leu Pro Ser Lys Gly Arg Glu			
180	185	190	
tct aat aat aag gct agt tcg ttc aga aga caa act ttt cat gct tta			1343
Ser Asn Asn Lys Ala Ser Ser Phe Arg Arg Gln Thr Phe His Ala Leu			
195	200	205	
tca cca act gac ctt atc aat gcg gcc aac aat gta acc ttg tca aag			1391
Ser Pro Thr Asp Leu Ile Asn Ala Asn Asn Val Thr Leu Ser Lys			
210	215	220	225
gac ttc caa tct gac atg cag aat ttt tct aag gct aag aaa ccg tct			1439
Asp Phe Gln Ser Asp Met Gln Asn Phe Ser Lys Ala Lys Lys Pro Ser			
230	235	240	
gta gga gct aac aat act gca aaa acc aga act caa tcc ata tct ttt			1487
Val Gly Ala Asn Asn Thr Ala Lys Thr Arg Thr Gln Ser Ile Ser Phe			
245	250	255	
gat aat act ccc tcc tca acg tca ttt ata ccc cca acc aat agt gtt			1535
Asp Asn Thr Pro Ser Ser Phe Ile Pro Pro Thr Asn Ser Val			
260	265	270	
tct gag aaa tta tcc gat ttc aaa ata gaa acc tcg aag gag gat ttg			1583
Ser Glu Lys Leu Ser Asp Phe Lys Ile Glu Thr Ser Lys Glu Asp Leu			
275	280	285	
att aat aaa act gca cca gct aaa aaa gag agt cct aca act tat ggt			1631
Ile Asn Lys Thr Ala Pro Ala Lys Lys Glu Ser Pro Thr Thr Tyr Gly			
290	295	300	305
gca gca tat cca tat ggg gga cct tta ctt caa cca aat cct att atg			1679
Ala Ala Tyr Pro Tyr Gly Gly Pro Leu Leu Gln Pro Asn Pro Ile Met			
310	315	320	
cca ggc cac cca cat aat ata tcc tcc cct atc tat ggt att aga tca			1727
Pro Gly His Pro His Asn Ile Ser Ser Pro Ile Tyr Gly Ile Arg Ser			
325	330	335	
cct ttt cct aat tct tat gaa atg ggc gcg caa ttt caa cct ttc tct			1775
Pro Phe Pro Asn Ser Tyr Glu Met Gly Ala Gln Phe Gln Pro Phe Ser			
340	345	350	

ccg att tta aat cct acg agt cat tca cta aat gca aat tct cca att Pro Ile Leu Asn Pro Thr Ser His Ser Leu Asn Ala Asn Ser Pro Ile 355 360 365	1823
cct cta acc caa tcg cca att cat ctt gca cca gtt tta aac cct agt Pro Leu Thr Gln Ser Pro Ile His Leu Ala Pro Val Leu Asn Pro Ser 370 375 380 385	1871
tca aat tct gtt gcc ttt tca gat atg aag aat gat ggt ggt aag ccc Ser Asn Ser Val Ala Phe Ser Asp Met Lys Asn Asp Gly Gly Lys Pro 390 395 400	1919
acc acc gat aac gac aag gcg ggt cca aat gtt agg atg gat tta ata Thr Thr Asp Asn Asp Lys Ala Gly Pro Asn Val Arg Met Asp Leu Ile 405 410 415	1967
aat cct aat ctt ggg cca tca atg caa cct ttc cac ata tta cct ccc Asn Pro Asn Leu Gly Pro Ser Met Gln Pro Phe His Ile Leu Pro Pro 420 425 430	2015
cag caa aac acc ccc cct ccc tgg ctt tat agc act cca cct ccc Gln Gln Asn Thr Pro Pro Pro Trp Leu Tyr Ser Thr Pro Pro Pro 435 440 445	2063
ttc aac gca atg gtt ccg cct cat ttg ttg gct caa aat cat atg ccg Phe Asn Ala Met Val Pro Pro His Leu Leu Ala Gln Asn His Met Pro 450 455 460 465	2111
tta atg aat agc gcc aat aat aaa cat cat ggt cgt aat aac aat agc Leu Met Asn Ser Ala Asn Asn Lys His His Gly Arg Asn Asn Asn Ser 470 475 480	2159
atg tca agt cat aat gac aat gac aac att ggt aat tct aat tac aac Met Ser Ser His Asn Asp Asn Asn Ile Gly Asn Ser Asn Tyr Asn 485 490 495	2207
aat aaa gac aca ggt cgt tct aac gtt ggt aaa atg aaa aat atg aaa Asn Lys Asp Thr Gly Arg Ser Asn Val Gly Lys Met Lys Asn Met Lys 500 505 510	2255
aac agt tat cat ggc tac tat aat aac aat aat aat aat aat aat aat Asn Ser Tyr His Gly Tyr Tyr Asn Asn Asn Asn Asn Asn Asn Asn Asn 515 520 525	2303
aac aat aat aat aat aac agt aat gct acc aac agc aac agc gcg gaa Asn Asn Asn Asn Asn Ser Asn Ala Thr Asn Ser Asn Ser Ala Glu 530 535 540 545	2351
aaa caa cgt aaa att gag gag tcg tcg aga ttt gcg gac gca gtt tta Lys Gln Arg Lys Ile Glu Glu Ser Ser Arg Phe Ala Asp Ala Val Leu 550 555 560	2399
gac caa tat atc gga agt att cac tca ttg tgt aaa gac caa cat ggt Asp Gln Tyr Ile Gly Ser Ile His Ser Leu Cys Lys Asp Gln His Gly 565 570 575	2447
tgt cgt ttt ctg caa aag cag ttg gat att ctc ggc agt aag gcg gcg Cys Arg Phe Leu Gln Lys Gln Leu Asp Ile Leu Gly Ser Lys Ala Ala 580 585 590	2495

gac cga att ttt gaa gaa act aag gat tat acg gtt gaa ttg atg act Asp Arg Ile Phe Glu Glu Thr Lys Asp Tyr Thr Val Glu Leu Met Thr 595 600 605	2543
gat tca ttc ggt aat tat ttg atc cag aag cta ttg gaa gag gtt acc Asp Ser Phe Gly Asn Tyr Leu Ile Gln Lys Leu Leu Glu Glu Val Thr 610 615 620 625	2591
aca gaa caa aga atc gta ctc aca aaa ata tct tcc cct cat ttt gtc Thr Glu Gln Arg Ile Val Leu Thr Lys Ile Ser Ser Pro His Phe Val 630 635 640	2639
gaa att tcc tta aac cct cat ggt act agg gca tta caa aaa ctc att Glu Ile Ser Leu Asn Pro His Gly Thr Arg Ala Leu Gln Lys Leu Ile 645 650 655	2687
gaa tgc atc aaa aca gat gaa gaa gca cag att gtt gtt gat tct tta Glu Cys Ile Lys Thr Asp Glu Ala Gln Ile Val Val Asp Ser Leu 660 665 670	2735
cgc cct tat act gtc cag ttg agt aag gat tta aat ggt aat cat gtt Arg Pro Tyr Thr Val Gln Leu Ser Lys Asp Leu Asn Gly Asn His Val 675 680 685	2783
att caa aaa tgt ttg caa agg ttg aag cct gaa aac ttc cag ttt atc Ile Gln Lys Cys Leu Gln Arg Leu Lys Pro Glu Asn Phe Gln Phe Ile 690 695 700 705	2831
ttt gac gca atc tct gat agc tgt att gat att gct act cat aga cac Phe Asp Ala Ile Ser Asp Ser Cys Ile Asp Ile Ala Thr His Arg His 710 715 720	2879
ggg tgt tgc gtt ttg caa cgt tgt cta gat cat ggg act aca gaa caa Gly Cys Cys Val Leu Gln Arg Cys Leu Asp His Gly Thr Thr Glu Gln 725 730 735	2927
tgt gac aat ctg tgt gat aag ttg cta gcc ctt gtt gat aaa tta act Cys Asp Asn Leu Cys Asp Lys Leu Leu Ala Leu Val Asp Lys Leu Thr 740 745 750	2975
ttg gat cca ttt ggc aac tat gtg gtg caa tat ata att acc aaa gag Leu Asp Pro Phe Gly Asn Tyr Val Val Gln Tyr Ile Ile Thr Lys Glu 755 760 765	3023
gct gag aag aac aaa tat gat tat acg cat aaa att gtc cac ctg ttg Ala Glu Lys Asn Lys Tyr Asp Tyr Thr His Lys Ile Val His Leu Leu 770 775 780 785	3071
aaa cca aga gcc atc gaa ctt tct atc cat aaa ttt gga tca aat gtg Lys Pro Arg Ala Ile Glu Leu Ser Ile His Lys Phe Gly Ser Asn Val 790 795 800	3119
att gaa aaa atc ttg aag aca gct att gtt tcg gag cca atg att ctg Ile Glu Lys Ile Leu Lys Thr Ala Ile Val Ser Glu Pro Met Ile Leu 805 810 815	3167
gaa att tta aat aat ggt ggc gag acg ggt att caa tca ttg ttg aat Glu Ile Leu Asn Asn Gly Gly Glu Thr Gly Ile Gln Ser Leu Leu Asn	3215

820

825

830

gat agc tac gga aat tac gtt tta cag aca gca tta gac att tct cat 3263
 Asp Ser Tyr Gly Asn Tyr Val Leu Gln Thr Ala Leu Asp Ile Ser His
 835 840 845

aag caa aat gac tat ctc tat aaa aga cta tca gag att gtg gcg cct 3311
 Lys Gln Asn Asp Tyr Leu Tyr Lys Arg Leu Ser Glu Ile Val Ala Pro
 850 855 860 865

tta ctg gtg ggc ccc ata aga aat aca cct cat ggt aaa aga atc atc 3359
 Leu Leu Val Gly Pro Ile Arg Asn Thr Pro His Gly Lys Arg Ile Ile
 870 875 880

gga atg tta cat tta gat tca tagttgatac atatatcctc agtttagctt 3410
 Gly Met Leu His Leu Asp Ser
 885

tttttacgtt agcctcatat aatatctttt gtacaatact aaaatacato attttttttt 3470
 tcgttgagga tcaaataaat atccaaagca aaaaaataat gaattttcac tttatggtat 3530
 actggtaaat agtgttgaag aaataagaga aggagatcgc cctagaaaaac agaatgttct 3590
 tatttaata agtaaactca aaagaaaaaa aaaaggaagg aagttttga gaacttttat 3650
 ctataacaaac gtatacgttt aactatctgg ataaacgtcg ctccacagga tactgttagag 3710
 gtcctcaaga tcaccgttat taacaaattc atctagtgcc cccaaattaa aactagttgc 3770
 agaaaaatttgg ttactgttgt tggtgttaat attgttaata ttgtttttat tggtgttgtt 3830
 gttgatttca ttgtgttca taaatggtaat ttgtactgaa gtgggttattt gctgctgagc 3890
 attgatttgtt ttatttagatt ggacttgcga attatgttc ccatttgttgc gttgcgcgtt 3950
 atcgggatttgc atcatatcag acacggataa tgacctaataa gaaggcaattt 4000

<210> 6

<211> 888

<212> PRT

<213> Saccharomyces cerevisiae

<400> 6

Met Ser Thr Lys Gly Leu Lys Glu Glu Ile Asp Asp Val Pro Ser Val
 1 5 10 15
 Asp Pro Val Val Ser Glu Thr Val Asn Ser Ala Leu Glu Gln Leu Gln
 20 25 30
 Leu Asp Asp Pro Glu Glu Asn Ala Thr Ser Asn Ala Phe Ala Asn Lys
 35 40 45
 Val Ser Gln Asp Ser Gln Phe Ala Asn Gly Pro Pro Ser Gln Met Phe
 50 55 60
 Pro His Pro Gln Met Met Gly Gly Met Gly Phe Met Pro Tyr Ser Gln
 65 70 75 80
 Met Met Gln Val Pro His Asn Pro Cys Pro Phe Phe Pro Pro Pro Asp
 85 90 95
 Phe Asn Asp Pro Thr Ala Pro Leu Ser Ser Pro Leu Asn Ala Gly
 100 105 110
 Gly Pro Pro Met Leu Phe Lys Asn Asp Ser Leu Pro Phe Gln Met Leu
 115 120 125
 Ser Ser Gly Ala Ala Val Ala Thr Gln Gly Gly Gln Asn Leu Asn Pro
 130 135 140
 Leu Ile Asn Asp Asn Ser Met Lys Val Leu Pro Ile Ala Ser Ala Asp
 145 150 155 160
 Pro Leu Trp Thr His Ser Asn Val Pro Gly Ser Ala Ser Val Ala Ile
 165 170 175
 Glu Glu Thr Thr Ala Thr Leu Gln Glu Ser Leu Pro Ser Lys Gly Arg
 180 185 190

Glu Ser Asn Asn Lys Ala Ser Ser Phe Arg Arg Gln Thr Phe His Ala
 195 200 205
 Leu Ser Pro Thr Asp Leu Ile Asn Ala Ala Asn Asn Val Thr Leu Ser
 210 215 220
 Lys Asp Phe Gln Ser Asp Met Gln Asn Phe Ser Lys Ala Lys Lys Pro
 225 230 235 240
 Ser Val Gly Ala Asn Asn Thr Ala Lys Thr Arg Thr Gln Ser Ile Ser
 245 250 255
 Phe Asp Asn Thr Pro Ser Ser Thr Ser Phe Ile Pro Pro Thr Asn Ser
 260 265 270
 Val Ser Glu Lys Leu Ser Asp Phe Lys Ile Glu Thr Ser Lys Glu Asp
 275 280 285
 Leu Ile Asn Lys Thr Ala Pro Ala Lys Lys Glu Ser Pro Thr Thr Tyr
 290 295 300
 Gly Ala Ala Tyr Pro Tyr Gly Gly Pro Leu Leu Gln Pro Asn Pro Ile
 305 310 315 320
 Met Pro Gly His Pro His Asn Ile Ser Ser Pro Ile Tyr Gly Ile Arg
 325 330 335
 Ser Pro Phe Pro Asn Ser Tyr Glu Met Gly Ala Gln Phe Gln Pro Phe
 340 345 350
 Ser Pro Ile Leu Asn Pro Thr Ser His Ser Leu Asn Ala Asn Ser Pro
 355 360 365
 Ile Pro Leu Thr Gln Ser Pro Ile His Leu Ala Pro Val Leu Asn Pro
 370 375 380
 Ser Ser Asn Ser Val Ala Phe Ser Asp Met Lys Asn Asp Gly Gly Lys
 385 390 395 400
 Pro Thr Thr Asp Asn Asp Lys Ala Gly Pro Asn Val Arg Met Asp Leu
 405 410 415
 Ile Asn Pro Asn Leu Gly Pro Ser Met Gln Pro Phe His Ile Leu Pro
 420 425 430
 Pro Gln Gln Asn Thr Pro Pro Pro Trp Leu Tyr Ser Thr Pro Pro
 435 440 445
 Pro Phe Asn Ala Met Val Pro Pro His Leu Leu Ala Gln Asn His Met
 450 455 460
 Pro Leu Met Asn Ser Ala Asn Asn Lys His His Gly Arg Asn Asn Asn
 465 470 475 480
 Ser Met Ser Ser His Asn Asp Asn Asp Asn Ile Gly Asn Ser Asn Tyr
 485 490 495
 Asn Asn Lys Asp Thr Gly Arg Ser Asn Val Gly Lys Met Lys Asn Met
 500 505 510
 Lys Asn Ser Tyr His Gly Tyr Tyr Asn Asn Asn Asn Asn Asn Asn
 515 520 525
 Asn Asn Asn Asn Asn Asn Ser Asn Ala Thr Asn Ser Asn Ser Ala
 530 535 540
 Glu Lys Gln Arg Lys Ile Glu Glu Ser Ser Arg Phe Ala Asp Ala Val
 545 550 555 560
 Leu Asp Gln Tyr Ile Gly Ser Ile His Ser Leu Cys Lys Asp Gln His
 565 570 575
 Gly Cys Arg Phe Leu Gln Lys Gln Leu Asp Ile Leu Gly Ser Lys Ala
 580 585 590
 Ala Asp Arg Ile Phe Glu Glu Thr Lys Asp Tyr Thr Val Glu Leu Met
 595 600 605
 Thr Asp Ser Phe Gly Asn Tyr Leu Ile Gln Lys Leu Leu Glu Glu Val
 610 615 620
 Thr Thr Glu Gln Arg Ile Val Leu Thr Lys Ile Ser Ser Pro His Phe
 625 630 635 640
 Val Glu Ile Ser Leu Asn Pro His Gly Thr Arg Ala Leu Gln Lys Leu
 645 650 655
 Ile Glu Cys Ile Lys Thr Asp Glu Glu Ala Gln Ile Val Val Asp Ser

	660	665	670
Leu Arg Pro Tyr Thr Val Gln Leu Ser Lys Asp Leu Asn Gly Asn His			
675	680	685	
Val Ile Gln Lys Cys Leu Gln Arg Leu Lys Pro Glu Asn Phe Gln Phe			
690	695	700	
Ile Phe Asp Ala Ile Ser Asp Ser Cys Ile Asp Ile Ala Thr His Arg			
705	710	715	720
His Gly Cys Cys Val Leu Gln Arg Cys Leu Asp His Gly Thr Thr Glu			
725	730	735	
Gln Cys Asp Asn Leu Cys Asp Lys Leu Leu Ala Leu Val Asp Lys Leu			
740	745	750	
Thr Leu Asp Pro Phe Gly Asn Tyr Val Val Gln Tyr Ile Ile Thr Lys			
755	760	765	
Glu Ala Glu Lys Asn Lys Tyr Asp Tyr Thr His Lys Ile Val His Leu			
770	775	780	
Leu Lys Pro Arg Ala Ile Glu Leu Ser Ile His Lys Phe Gly Ser Asn			
785	790	795	800
Val Ile Glu Lys Ile Leu Lys Thr Ala Ile Val Ser Glu Pro Met Ile			
805	810	815	
Leu Glu Ile Leu Asn Asn Gly Glu Thr Gly Ile Gln Ser Leu Leu			
820	825	830	
Asn Asp Ser Tyr Gly Asn Tyr Val Leu Gln Thr Ala Leu Asp Ile Ser			
835	840	845	
His Lys Gln Asn Asp Tyr Leu Tyr Lys Arg Leu Ser Glu Ile Val Ala			
850	855	860	
Pro Leu Leu Val Gly Pro Ile Arg Asn Thr Pro His Gly Lys Arg Ile			
865	870	875	880
Ile Gly Met Leu His Leu Asp Ser			
	885		

<210> 7
<211> 5319
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (57) ... (3614)
<223> D43951

<400> 7
gaagatcgaaat ccatcttcat cctaccgctc cgcccggttt ggtgga atg 59
Met
1

agc gtt gca tgc ttg aag aga aaa gca gtg ctt tgg cag gac tct 107
Ser Val Ala Cys Val Leu Lys Arg Lys Ala Val Leu Trp Gln Asp Ser
5 10 15

tcc agc ccc cac ctg aaa cat cac cct caa gaa cca gct aat ccc aac 155
Phe Ser Pro His Leu Lys His Pro Gln Glu Pro Ala Asn Pro Asn
20 25 30

atg cct gtt ttg aca tct gga aca ggg tcg caa gcg cag cca caa 203
Met Pro Val Val Leu Thr Ser Gly Thr Gly Ser Gln Ala Gln Pro Gln
35 40 45

cca gct gca aat cag gct ctt gca gct ggg act cac tcc agc cct gtc 251

Pro Ala Ala Asn Gln Ala Leu Ala Ala Gly Thr His Ser Ser Pro Val			
50	55	60	65
cca gga tct ata gga gtt gca ggc cgt tcc cag gac gac gct atg gtg			299
Pro Gly Ser Ile Gly Val Ala Gly Arg Ser Gln Asp Asp Ala Met Val			
70	75	80	
gac tac ttc ttt cag agg cag cat ggt gag cag ctt ggg gga gga gga			347
Asp Tyr Phe Phe Gln Arg Gln His Gly Glu Gln Leu Gly Gly Gly			
85	90	95	
agt gga gga ggc ggc tat aat aat agc aaa cat cga tgg cct act ggg			395
Ser Gly Gly Gly Tyr Asn Asn Ser Lys His Arg Trp Pro Thr Gly			
100	105	110	
gat aac att cat gca gaa cat cag gtg cgt tcc atg gat gaa ctg aat			443
Asp Asn Ile His Ala Glu His Gln Val Arg Ser Met Asp Glu Leu Asn			
115	120	125	
cat gat ttt caa gca ctt gct ctg gag gga aga gcg atg gga gag cag			491
His Asp Phe Gln Ala Leu Ala Leu Glu Gly Arg Ala Met Gly Glu Gln			
130	135	140	145
ctc ttg cca ggt aaa aag ttt tgg gaa aca gat gaa tcc agc aaa gat			539
Leu Leu Pro Gly Lys Phe Trp Glu Thr Asp Glu Ser Ser Lys Asp			
150	155	160	
gga cca aaa gga ata ttc ctg ggt gat caa tgg cga gac agt gcc tgg			587
Gly Pro Lys Gly Ile Phe Leu Gly Asp Gln Trp Arg Asp Ser Ala Trp			
165	170	175	
gga aca tca gat cat tca gtt tcc cag cca atc atg gtg cag aga aga			635
Gly Thr Ser Asp His Ser Val Ser Gln Pro Ile Met Val Gln Arg Arg			
180	185	190	
cct ggt cag agt ttc cat gtg aac agt gag gtc aat tct gta ctg tcc			683
Pro Gly Gln Ser Phe His Val Asn Ser Glu Val Asn Ser Val Leu Ser			
195	200	205	
cca cga tcg gag agt ggg gga cta ggc gtt agc atg gtg gag tat gtg			731
Pro Arg Ser Glu Ser Gly Gly Leu Gly Val Ser Met Val Glu Tyr Val			
210	215	220	225
ttg agc tca tcc ccg ggc gat tcc tgt cta aga aaa gga gga ttt ggc			779
Leu Ser Ser Pro Gly Asp Ser Cys Leu Arg Lys Gly Gly Phe Gly			
230	235	240	
cca agg gat gca gac agt gat gaa aac gac aaa ggt gaa aag aag aac			827
Pro Arg Asp Ala Asp Ser Asp Glu Asn Asp Lys Gly Glu Lys Lys Asn			
245	250	255	
aag ggt acg ttt gat gga gat aag cta gga gat ttg aag gag gag ggt			875
Lys Gly Thr Phe Asp Gly Asp Lys Leu Gly Asp Leu Lys Glu Glu Gly			
260	265	270	
gat gtg atg gac aag acc aat ggt tta cca gtg cag aat ggg att gat			923
Asp Val Met Asp Lys Thr Asn Gly Leu Pro Val Gln Asn Gly Ile Asp			
275	280	285	

gca gac gtc aaa gat ttt agc cgt acc cct ggt aat tgc cag aac tct Ala Asp Val Lys Asp Phe Ser Arg Thr Pro Gly Asn Cys Gln Asn Ser 290 295 300 305	971
gct aat gaa gtg gat ctt ctg ggt cca aac cag aat ggt tct gag ggc Ala Asn Glu Val Asp Leu Leu Gly Pro Asn Gln Asn Gly Ser Glu Gly 310 315 320	1019
tta gcc cag ctg acc agc acc aat ggt gcc aag cct gtg gag gat ttc Leu Ala Gln Leu Thr Ser Thr Asn Gly Ala Lys Pro Val Glu Asp Phe 325 330 335	1067
tcc aac atg gag tcc cag agt gtc ccc ttg gac ccc atg gaa cat gtg Ser Asn Met Glu Ser Gln Ser Val Pro Leu Asp Pro Met Glu His Val 340 345 350	1115
ggc atg gag cct ctt cag ttt gat tat tca ggc acg cag gta cct gtg Gly Met Glu Pro Leu Gln Phe Asp Tyr Ser Gly Thr Gln Val Pro Val 355 360 365	1163
gac tca gca gca gca act gtg gga ctt ttt gac tac aat tct caa caa Asp Ser Ala Ala Ala Thr Val Gly Leu Phe Asp Tyr Asn Ser Gln Gln 370 375 380 385	1211
cag ctg ttc caa aga cct aat gcg ctt gct gtc cag cag ttg aca gct Gln Leu Phe Gln Arg Pro Asn Ala Leu Ala Val Gln Gln Leu Thr Ala 390 395 400	1259
gct cag cag cag tat gca ctg gca gct gct cat cag ccg cac atc Ala Gln Gln Gln Tyr Ala Leu Ala Ala His Gln Pro His Ile 405 410 415	1307
ggt tta gct ccc gct gcg ttt gtc ccc aat cca tac atc atc agc gct Gly Leu Ala Pro Ala Ala Phe Val Pro Asn Pro Tyr Ile Ile Ser Ala 420 425 430	1355
gct ccc cca ggg acg gac ccc tac aca gct gga ttg gct gca gca gcg Ala Pro Pro Gly Thr Asp Pro Tyr Thr Ala Gly Leu Ala Ala Ala Ala 435 440 445	1403
aca cta ggc cca gct gtg gtc cct cac cag tat tat gga gtt act ccc Thr Leu Gly Pro Ala Val Val Pro His Gln Tyr Tyr Gly Val Thr Pro 450 455 460 465	1451
tgg gga gtc tac cct gcc agt ctt ttc cag cag caa gct gcc gct gcc Trp Gly Val Tyr Pro Ala Ser Leu Phe Gln Gln Ala Ala Ala Ala 470 475 480	1499
gct gca gca act aat tca gct aat caa cag acc acc cca cag gct cag Ala Ala Ala Thr Asn Ser Ala Asn Gln Gln Thr Thr Pro Gln Ala Gln 485 490 495	1547
caa gga cag cag cag gtt ctc cgt gga gga gcc agc caa cgt cct ttg Gln Gly Gln Gln Val Leu Arg Gly Gly Ala Ser Gln Arg Pro Leu 500 505 510	1595
acc cca aac cag aac cag cag gga cag caa acg gat ccc ctt gtg gca Thr Pro Asn Gln Asn Gln Gln Gly Gln Gln Thr Asp Pro Leu Val Ala 515 520 525	1643

gct gca gca gtg aat tct gcc ctt gca ttt gga caa ggt ctg gca gca Ala Ala Ala Val Asn Ser Ala Leu Ala Phe Gly Gln Gly Leu Ala Ala 530 535 540 545	1691
ggc atg cca ggt tat ccg gtg ttg gct cct gct gct tac tat gac caa Gly Met Pro Gly Tyr Pro Val Leu Ala Pro Ala Ala Tyr Tyr Asp Gln 550 555 560	1739
act ggt gcc ctt gta gtg aat gca ggc gcg aga aat ggt ctt gga gct Thr Gly Ala Leu Val Val Asn Ala Gly Ala Arg Asn Gly Leu Gly Ala 565 570 575	1787
cct gtt cga ctt gta gct cct gcc cca gtc atc att agt tcc tca gct Pro Val Arg Leu Val Ala Pro Ala Pro Val Ile Ile Ser Ser Ser Ala 580 585 590	1835
gca caa gca gct gtt gca gca gcc gca gct tca gca aat gga gca gct Ala Gln Ala Ala Val Ala Ala Ala Ser Ala Asn Gly Ala Ala 595 600 605	1883
ggt ggt ctt gct gga aca aca aat gga cca ttt cgc cct tta gga aca Gly Gly Leu Ala Gly Thr Thr Asn Gly Pro Phe Arg Pro Leu Gly Thr 610 615 620 625	1931
cag cag cct cag ccc cag ccc cag cag ccc aat aac aac ctg gca Gln Gln Pro Gln Pro Gln Gln Gln Pro Asn Asn Asn Leu Ala 630 635 640	1979
tcc agt tct ttc tac ggc aac aac tct ctg aac agc aat tca cag agc Ser Ser Ser Phe Tyr Gly Asn Asn Ser Leu Asn Ser Asn Ser Gln Ser 645 650 655	2027
agc tcc ctc ttc tcc cag ggc tct gcc cag cct gcc aac aca tcc ttg Ser Ser Leu Phe Ser Gln Gly Ser Ala Gln Pro Ala Asn Thr Ser Leu 660 665 670	2075
gga ttc gga agt agc agt tct ctc ggc gcc acc ctg gga tcc gcc ctt Gly Phe Gly Ser Ser Ser Leu Gly Ala Thr Leu Gly Ser Ala Leu 675 680 685	2123
gga ggg ttt gga aca gca gtt gca aac tcc aac act ggc agt ggc tcc Gly Gly Phe Gly Thr Ala Val Ala Asn Ser Asn Thr Gly Ser Gly Ser 690 695 700 705	2171
cgc cgt gac tcc ctg act ggc agc agt gac ctt tat aag agg aca tcg Arg Arg Asp Ser Leu Thr Gly Ser Ser Asp Leu Tyr Lys Arg Thr Ser 710 715 720	2219
agc agc ttg acc ccc att gga cac agt ttt tat aac ggc ctt agc ttt Ser Ser Leu Thr Pro Ile Gly His Ser Phe Tyr Asn Gly Leu Ser Phe 725 730 735	2267
tcc tcc tct cct gga ccc gtg ggc atg cct ctc cct agt cag gga cca Ser Ser Ser Pro Gly Pro Val Gly Met Pro Leu Pro Ser Gln Gly Pro 740 745 750	2315
gga cat tca cag aca cca cct cct tcc ctc tct tca cat gga tcc tct Gly His Ser Gln Thr Pro Pro Ser Leu Ser Ser His Gly Ser Ser	2363

755

760

765

tca agc tta aac ctg gga gga ctc acg aat ggc agt gga aga tac atc Ser Ser Leu Asn Leu Gly Gly Leu Thr Asn Gly Ser Gly Arg Tyr Ile 770 775 780 785	2411
tct gct gct cca ggc gct gaa gcc aag tac cgc agt gca agc agc gcc Ser Ala Ala Pro Gly Ala Glu Ala Lys Tyr Arg Ser Ala Ser Ser Ala 790 795 800	2459
tcc agc ctc ttc agc ccg agc agc act ctt ttc tct tcc tct cgt ttg Ser Ser Leu Phe Ser Pro Ser Ser Thr Leu Phe Ser Ser Ser Arg Leu 805 810 815	2507
cga tat gga atg tct gat gtc atg cct tct ggc agg agc agg ctt ttg Arg Tyr Gly Met Ser Asp Val Met Pro Ser Gly Arg Ser Arg Leu Leu 820 825 830	2555
gaa gat ttt cga aac aac cgg tac ccc aat tta caa ctg cgg gag att Glu Asp Phe Arg Asn Asn Arg Tyr Pro Asn Leu Gln Leu Arg Glu Ile 835 840 845	2603
gct gga cat ata atg gaa ttt tcc caa gac cag cat ggg tcc aga ttc Ala Gly His Ile Met Glu Phe Ser Gln Asp Gln His Gly Ser Arg Phe 850 855 860 865	2651
att cag ctg aaa ctg gag cgt gcc aca cca gct gag cgc cag ctt gtc Ile Gln Leu Lys Leu Glu Arg Ala Thr Pro Ala Glu Arg Gln Leu Val 870 875 880	2699
ttc aat gaa atc ctc cag gct gcc tac caa ctc atg gtg gat gtg ttt Phe Asn Glu Ile Leu Gln Ala Ala Tyr Gln Leu Met Val Asp Val Phe 885 890 895	2747
ggt aat tac gtc att cag aag ttc ttt gaa ttt ggc agt ctt gaa cag Gly Asn Tyr Val Ile Gln Lys Phe Phe Glu Phe Gly Ser Leu Glu Gln 900 905 910	2795
aag ctg gct ttg gca gaa cgg att cga ggc cac gtc ctg tca ttg gca Lys Ile Ala Leu Ala Glu Arg Ile Arg Gly His Val Leu Ser Leu Ala 915 920 925	2843
cta cag atg tat ggc tgc cgt gtt atc cag aaa gct ctt gag ttt att Leu Gln Met Tyr Gly Cys Arg Val Ile Gln Lys Ala Leu Glu Phe Ile 930 935 940 945	2891
cct tca gac cag cag aat gag atg gtt cg gaa cta gat ggc cat gtc Pro Ser Asp Gln Gln Asn Glu Met Val Arg Glu Leu Asp Gly His Val 950 955 960	2939
ttg aag tgt gtg aaa gat cag aat ggc aat cac gtg gtt cag aaa tgc Leu Lys Cys Val Lys Asp Gln Asn Gly Asn His Val Val Gln Lys Cys 965 970 975	2987
att gaa tgt gta cag ccc cag tct ttg caa ttt atc atc gat ggc ttt Ile Glu Cys Val Gln Pro Gln Ser Leu Gln Phe Ile Ile Asp Ala Phe 980 985 990	3035
aag gga cag gta ttt gcc tta tcc aca cat cct tat ggc tgc cga gtg	3083

Lys Gly Gln Val Phe Ala Leu Ser Thr His Pro Tyr Gly Cys Arg Val
 995 1000 1005

att cag aga atc ctg gag cac tgt ctc cct gac cag aca ctc cct att 3131
 Ile Gln Arg Ile Leu Glu His Cys Leu Pro Asp Gln Thr Leu Pro Ile
 1010 1015 1020 1025

tta gag gag ctt cac cag cac aca gag cag ctt gta cag gat caa tat 3179
 Leu Glu Glu Leu His Gln His Thr Glu Gln Leu Val Gln Asp Gln Tyr
 1030 1035 1040

gga aat tat gta atc caa cat gta ctg gag cac ggt cgt cct gag gat 3227
 Gly Asn Tyr Val Ile Gln His Val Leu Glu His Gly Arg Pro Glu Asp
 1045 1050 1055

aaa agc aaa att gta gca gaa atc cga ggc aat gta ctt gta ttg agt 3275
 Lys Ser Lys Ile Val Ala Glu Ile Arg Gly Asn Val Leu Val Leu Ser
 1060 1065 1070

cag cac aaa ttt gca agc aat gtt gtg gag aag tgt gtt act cac gcc 3323
 Gln His Lys Phe Ala Ser Asn Val Val Glu Lys Cys Val Thr His Ala
 1075 1080 1085

tca cgt acg gag cgc gct gtg ctc atc gat gag gtg tgc acc atg aac 3371
 Ser Arg Thr Glu Arg Ala Val Leu Ile Asp Glu Val Cys Thr Met Asn
 1090 1095 1100 1105

gac ggt ccc cac agt gcc tta tac acc atg atg aag gac cag tat gcc 3419
 Asp Gly Pro His Ser Ala Leu Tyr Thr Met Met Lys Asp Gln Tyr Ala
 1110 1115 1120

aac tac gtg gtc cag aag atg att gac gtg gcg gag cca ggc cag cgg 3467
 Asn Tyr Val Val Gln Lys Met Ile Asp Val Ala Glu Pro Gly Gln Arg
 1125 1130 1135

aag atc gtc atg cat aag atc cgg ccc cac atc gca act ctt cgt aag 3515
 Lys Ile Val Met His Lys Ile Arg Pro His Ile Ala Thr Leu Arg Lys
 1140 1145 1150

tac acc tat ggc aag cac att ctg gcc aag ctg gag aag tac tac atg 3563
 Tyr Thr Tyr Gly Lys His Ile Leu Ala Lys Leu Glu Lys Tyr Tyr Met
 1155 1160 1165

aag aac ggt gtt gac tta ggg ccc atc tgt ggc ccc cct aat ggt atc 3611
 Lys Asn Gly Val Asp Leu Gly Pro Ile Cys Gly Pro Pro Asn Gly Ile
 1170 1175 1180 1185

atc tgaggcagtgc tcacccgctg ttccctcatt cccgctgacc tcactggccc 3664
 Ile

actggcaaata ccaaccagca accagaaatg ttcttagtgta gaggctgaga cggggcaagtg 3724
 gttgctccag gattactccc tcctccaaaa aaggaatcaa atccacgagt ggaaaaagcct 3784
 ttgttaattt aatttttatta cacataacat gtactatattt tttaatttga ctaattgccc 3844
 tgctgttttta ctgggttata ggatacttgt acataggtaa ccaatgtaca tggggaggcca 3904
 catatttgt tcactgttgt atctatattt cacatgttga aaccttcagg gtgggtgggt 3964
 taacaaaaaaa aaaaagctt aaaaaaaaaa gaaaaaaaaagg aaaaggttt tagctcattt 4024
 gcctggccgg caagtttgc aaatagctct tccccacctc ctcatttttag taaaaaacaa 4084
 acaaaaaacaa aaaaacctga gaagttgaa ttgttagttaa atgaccccaa actggcattt 4144

aacactgttt	ataaaaaaaaata	tatataaaaaata	tatataaaaaata	taatgaaaaaa	gttttcagag	4204
ttgctaaagc	ttcagtttgt	gacattaagt	ttatgaaaatt	ctaaaaaaatg	ccttttttgg	4264
agactatatt	atgctgaaga	aggctgttcg	tgaggaggag	atgcgac	ccagaacgtc	4324
tttgagggct	gggcgggtgt	gattgtttac	tgccctactgg	attttttct	attaacatgt	4384
aaaggtaaaa	tctgatttatt	tagcatgaga	aaaaaaaaatcc	aactctgctt	ttggcttgc	4444
ttctataaaat	atatagtgtt	tacttggtgt	agactttgc	tatatacaaa	ttttagtat	4504
tttctgtttt	tgatgtctaa	tctgtatcta	taatgtacc	tagtagtcg	acataacttt	4564
gattgtacaa	ttgtacattt	gtataccgt	aatgtaaaatg	tggagaagtt	tgaatcaaca	4624
taaacacgtt	tttggtaag	aaaagagaat	tagccagccc	tgtgcattca	gtgttatattc	4684
tcaccttttta	tggcgttagc	atatagtgtt	gtatattgtt	aattgttaatt	tcaaccagaa	4744
gtaaaattttt	ttgttttggaa	ggaataaaatg	ttctttatac	agcctagttt	atgtttaaaa	4804
agaaaaaaaaat	agcttggttt	tatttgcatt	ctagtctcaa	gtatacgag	attctttctt	4864
aatgttattc	aagattgagt	tctcaactgt	gtttttttaa	tcctaaaaaa	gtaatgtttt	4924
gattttgtga	cagtcaaaag	gacgtgc	aaatgtctagcc	tgccccagct	tcccttacaa	4984
tcagagcccc	tctcacccctt	taaagtgtga	atcgcccttc	ccttttgc	agaagatgaa	5044
ctgtattttt	cattttgtct	acttgcatt	gaatgtaaaca	tactgtcaat	tttccttgg	5104
tgaatataaga	attgtacac	tacacgggt	acatttccag	agcctgtgt	atatttccaa	5164
tgaactttttt	tgcaaggcaca	cttgcacca	tatgtgtata	attaacaaac	ctgtgtatgc	5224
ttatgcctgg	gcaactattt	tttgcacca	tttgtgttagat	tgtctctaaa	caatgtgtga	5284
tctttatTTT	gaaaaataca	gaacttttgg	atctg			5319

```
<210> 8  
<211> 1186  
<212> PRT  
<213> Homo sapiens
```

```

<400> 8
Met Ser Val Ala Cys Val Leu Lys Arg Lys Ala Val Leu Trp Gln Asp
  1           5           10          15
Ser Phe Ser Pro His Leu Lys His His Pro Gln Glu Pro Ala Asn Pro
  20          25          30
Asn Met Pro Val Val Leu Thr Ser Gly Thr Gly Ser Gln Ala Gln Pro
  35          40          45
Gln Pro Ala Ala Asn Gln Ala Leu Ala Ala Gly Thr His Ser Ser Pro
  50          55          60
Val Pro Gly Ser Ile Gly Val Ala Gly Arg Ser Gln Asp Asp Ala Met
  65          70          75          80
Val Asp Tyr Phe Phe Gln Arg Gln His Gly Glu Gln Leu Gly Gly Gly
  85          90          95
Gly Ser Gly Gly Gly Tyr Asn Asn Ser Lys His Arg Trp Pro Thr
  100         105         110
Gly Asp Asn Ile His Ala Glu His Gln Val Arg Ser Met Asp Glu Leu
  115         120         125
Asn His Asp Phe Gln Ala Leu Ala Leu Glu Gly Arg Ala Met Gly Glu
  130         135         140
Gln Leu Leu Pro Gly Lys Lys Phe Trp Glu Thr Asp Glu Ser Ser Lys
  145         150         155         160
Asp Gly Pro Lys Gly Ile Phe Leu Gly Asp Gln Trp Arg Asp Ser Ala
  165         170         175
Trp Gly Thr Ser Asp His Ser Val Ser Gln Pro Ile Met Val Gln Arg
  180         185         190
Arg Pro Gly Gln Ser Phe His Val Asn Ser Glu Val Asn Ser Val Leu
  195         200         205
Ser Pro Arg Ser Glu Ser Gly Gly Leu Gly Val Ser Met Val Glu Tyr
  210         215         220
Val Leu Ser Ser Ser Pro Gly Asp Ser Cys Leu Arg Lys Gly Gly Phe
  225         230         235         240
Gly Pro Arg Asp Ala Asp Ser Asp Glu Asn Asp Lys Gly Glu Lys Lys
  245         250         255

```

Asn Lys Gly Thr Phe Asp Gly Asp Lys Leu Gly Asp Leu Lys Glu Glu
 260 265 270
 Gly Asp Val Met Asp Lys Thr Asn Gly Leu Pro Val Gln Asn Gly Ile
 275 280 285
 Asp Ala Asp Val Lys Asp Phe Ser Arg Thr Pro Gly Asn Cys Gln Asn
 290 295 300
 Ser Ala Asn Glu Val Asp Leu Leu Gly Pro Asn Gln Asn Gly Ser Glu
 305 310 315 320
 Gly Leu Ala Gln Leu Thr Ser Thr Asn Gly Ala Lys Pro Val Glu Asp
 325 330 335
 Phe Ser Asn Met Glu Ser Gln Ser Val Pro Leu Asp Pro Met Glu His
 340 345 350
 Val Gly Met Glu Pro Leu Gln Phe Asp Tyr Ser Gly Thr Gln Val Pro
 355 360 365
 Val Asp Ser Ala Ala Ala Thr Val Gly Leu Phe Asp Tyr Asn Ser Gln
 370 375 380
 Gln Gln Leu Phe Gln Arg Pro Asn Ala Leu Ala Val Gln Gln Leu Thr
 385 390 395 400
 Ala Ala Gln Gln Gln Tyr Ala Leu Ala Ala Ala His Gln Pro His
 405 410 415
 Ile Gly Leu Ala Pro Ala Ala Phe Val Pro Asn Pro Tyr Ile Ile Ser
 420 425 430
 Ala Ala Pro Pro Gly Thr Asp Pro Tyr Thr Ala Gly Leu Ala Ala Ala
 435 440 445
 Ala Thr Leu Gly Pro Ala Val Val Pro His Gln Tyr Tyr Gly Val Thr
 450 455 460
 Pro Trp Gly Val Tyr Pro Ala Ser Leu Phe Gln Gln Gln Ala Ala Ala
 465 470 475 480
 Ala Ala Ala Ala Thr Asn Ser Ala Asn Gln Gln Thr Thr Pro Gln Ala
 485 490 495
 Gln Gln Gly Gln Gln Val Leu Arg Gly Gly Ala Ser Gln Arg Pro
 500 505 510
 Leu Thr Pro Asn Gln Asn Gln Gly Gln Gln Thr Asp Pro Leu Val
 515 520 525
 Ala Ala Ala Ala Val Asn Ser Ala Leu Ala Phe Gly Gln Gly Leu Ala
 530 535 540
 Ala Gly Met Pro Gly Tyr Pro Val Leu Ala Pro Ala Ala Tyr Tyr Asp
 545 550 555 560
 Gln Thr Gly Ala Leu Val Val Asn Ala Gly Ala Arg Asn Gly Leu Gly
 565 570 575
 Ala Pro Val Arg Leu Val Ala Pro Ala Pro Val Ile Ile Ser Ser Ser
 580 585 590
 Ala Ala Gln Ala Ala Val Ala Ala Ala Ala Ser Ala Asn Gly Ala
 595 600 605
 Ala Gly Gly Leu Ala Gly Thr Thr Asn Gly Pro Phe Arg Pro Leu Gly
 610 615 620
 Thr Gln Gln Pro Gln Pro Gln Gln Gln Pro Asn Asn Asn Leu
 625 630 635 640
 Ala Ser Ser Ser Phe Tyr Gly Asn Asn Ser Leu Asn Ser Asn Ser Gln
 645 650 655
 Ser Ser Ser Leu Phe Ser Gln Gly Ser Ala Gln Pro Ala Asn Thr Ser
 660 665 670
 Leu Gly Phe Gly Ser Ser Ser Leu Gly Ala Thr Leu Gly Ser Ala
 675 680 685
 Leu Gly Gly Phe Gly Thr Ala Val Ala Asn Ser Asn Thr Gly Ser Gly
 690 695 700
 Ser Arg Arg Asp Ser Leu Thr Gly Ser Ser Asp Leu Tyr Lys Arg Thr
 705 710 715 720
 Ser Ser Ser Leu Thr Pro Ile Gly His Ser Phe Tyr Asn Gly Leu Ser

725	730	735
Phe Ser Ser Ser Pro Gly Pro Val Gly	Met Pro Leu Pro Ser Gln Gly	
740	745	750
Pro Gly His Ser Gln Thr Pro Pro Pro Ser Leu Ser Ser His Gly Ser		
755	760	765
Ser Ser Ser Leu Asn Leu Gly Gly Leu Thr Asn Gly Ser Gly Arg Tyr		
770	775	780
Ile Ser Ala Ala Pro Gly Ala Glu Ala Lys Tyr Arg Ser Ala Ser Ser		
785	790	800
Ala Ser Ser Leu Phe Ser Pro Ser Ser Thr Leu Phe Ser Ser Ser Arg		
805	810	815
Leu Arg Tyr Gly Met Ser Asp Val Met Pro Ser Gly Arg Ser Arg Leu		
820	825	830
Leu Glu Asp Phe Arg Asn Asn Arg Tyr Pro Asn Leu Gln Leu Arg Glu		
835	840	845
Ile Ala Gly His Ile Met Glu Phe Ser Gln Asp Gln His Gly Ser Arg		
850	855	860
Phe Ile Gln Leu Lys Leu Glu Arg Ala Thr Pro Ala Glu Arg Gln Leu		
865	870	880
Val Phe Asn Glu Ile Leu Gln Ala Ala Tyr Gln Leu Met Val Asp Val		
885	890	895
Phe Gly Asn Tyr Val Ile Gln Lys Phe Phe Glu Phe Gly Ser Leu Glu		
900	905	910
Gln Lys Leu Ala Leu Ala Glu Arg Ile Arg Gly His Val Leu Ser Leu		
915	920	925
Ala Leu Gln Met Tyr Gly Cys Arg Val Ile Gln Lys Ala Leu Glu Phe		
930	935	940
Ile Pro Ser Asp Gln Gln Asn Glu Met Val Arg Glu Leu Asp Gly His		
945	950	960
Val Leu Lys Cys Val Lys Asp Gln Asn Gly Asn His Val Val Gln Lys		
965	970	975
Cys Ile Glu Cys Val Gln Pro Gln Ser Leu Gln Phe Ile Ile Asp Ala		
980	985	990
Phe Lys Gly Gln Val Phe Ala Leu Ser Thr His Pro Tyr Gly Cys Arg		
995	1000	1005
Val Ile Gln Arg Ile Leu Glu His Cys Leu Pro Asp Gln Thr Leu Pro		
1010	1015	1020
Ile Leu Glu Glu Leu His Gln His Thr Glu Gln Leu Val Gln Asp Gln		
1025	1030	1040
Tyr Gly Asn Tyr Val Ile Gln His Val Leu Glu His Gly Arg Pro Glu		
1045	1050	1055
Asp Lys Ser Lys Ile Val Ala Glu Ile Arg Gly Asn Val Leu Val Leu		
1060	1065	1070
Ser Gln His Lys Phe Ala Ser Asn Val Val Glu Lys Cys Val Thr His		
1075	1080	1085
Ala Ser Arg Thr Glu Arg Ala Val Leu Ile Asp Glu Val Cys Thr Met		
1090	1095	1100
Asn Asp Gly Pro His Ser Ala Leu Tyr Thr Met Met Lys Asp Gln Tyr		
1105	1110	1120
Ala Asn Tyr Val Val Gln Lys Met Ile Asp Val Ala Glu Pro Gly Gln		
1125	1130	1135
Arg Lys Ile Val Met His Lys Ile Arg Pro His Ile Ala Thr Leu Arg		
1140	1145	1150
Lys Tyr Thr Tyr Gly Lys His Ile Leu Ala Lys Leu Glu Lys Tyr Tyr		
1155	1160	1165
Met Lys Asn Gly Val Asp Leu Gly Pro Ile Cys Gly Pro Pro Asn Gly		
1170	1175	1180
Ile Ile		
1185		

<210> 9
 <211> 2112
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (419) ... (1942)
 <223> D13645

 <400> 9
 ggaagttaaa gggaaaaaggc aattcacagg aaagagtaca aagacacgcac aagaaaaaaaaa 60
 cagatttcat aaaaatagtg attctgggtc ttccaaagaca tttccaacaa ggaaagttgc 120
 taaagaaggt ggacctaaag tcacatctag gaacttttag gaaagttatca caaaacttgg 180
 gaaaaagggt gttaaaggcgt tcaagaataa gcagcaaggg gacaaatcac caaagaacaa 240
 attccagccg gcaaataaat tcaacaagaa gagaaaattc cagccagatg gttagaagcga 300
 tgaatcagca gccaaaggc ccaaataatggc tgacttcaaa aagaagaaga aagaactgaa 360
 gcaaaggcaga caactcgatg ataaaaaccaa ctatgacatt gttgttcggg caaaggcag 418
 atg tgg gag att tta aga aga aaa gac tgt gac aaa gaa aaa aga gta 466
 aag tta atg agt gat ttg cag aag ttg att caa ggg aaa att aaa act 514
 Met Trp Glu Ile Leu Arg Arg Lys Asp Cys Asp Lys Glu Lys Arg Val
 1 5 10 15

 att gca ttt gca cac gat tca act cgt gtg atc cag tgt tac att cag 562
 Lys Leu Met Ser Asp Leu Gln Lys Leu Ile Gln Gly Lys Ile Lys Thr
 20 25 30

 tat ggt aat gaa gaa cag aga aaa cag gct ttt gaa gaa ttg cga gat 610
 Ile Ala Phe Ala His Asp Ser Thr Arg Val Ile Gln Cys Tyr Ile Gln
 35 40 45

 gat ttg gtt gag tta agt aaa gcc aaa tat tcg aga aat att gtt aag 658
 Tyr Gly Asn Glu Glu Gln Arg Lys Gln Ala Phe Glu Glu Leu Arg Asp
 50 55 60

 aaa ttt ctc atq tat gga agt aaa cca cag att gca gag ata atc aga 706
 Asp Leu Val Glu Leu Ser Lys Ala Lys Tyr Ser Arg Asn Ile Val Lys
 65 70 75 80

 agt ttt aaa ggc cac gtg agg aag atg ctg cggt cat gcg gaa gca tca 754
 Lys Phe Leu Met Tyr Gly Ser Lys Pro Gln Ile Ala Glu Ile Ile Arg
 85 90 95

 gcc atc gtg gag tac gca tac aat gac aaa gcc att ttg gag cag agg 802
 Ser Phe Lys Gly His Val Arg Lys Met Leu Arg His Ala Glu Ala Ser
 100 105 110

 aac atg ctg acg gaa gag ctc tat ggg aac aca ttt cag ctt tac aag 850
 Ala Ile Val Glu Tyr Ala Tyr Asn Asp Lys Ala Ile Leu Glu Gln Arg
 115 120 125

 tca gca gat cac cga act ctg gac aaa gtg tta gag gta cag cca gaa 898
 Asn Met Leu Thr Glu Glu Leu Tyr Gly Asn Thr Phe Gln Leu Tyr Lys
 130 135 140

 aaa tta gaa ctt att atg gat gaa atg aaa cag att cta act cca atg 946
 Ser Ala Asp His Arg Thr Leu Asp Lys Val Leu Glu Val Gln Pro Glu
 145 150 155 160

gcc caa aag gaa gct gtg att aag cac tca ttg gtg cat aaa gta ttc Lys Leu Glu Leu Ile Met Asp Glu Met Lys Gln Ile Leu Thr Pro Met 165 170 175	994
ttg gac ttt ttt acc tat gca ccc ccc aaa ctc aga tca gaa atg att Ala Gln Lys Glu Ala Val Ile Lys His Ser Leu Val His Lys Val Phe 180 185 190	1042
gaa gcc atc cgc gaa gcg gtg gtc tac ctg gca cac aca cac gat ggc Leu Asp Phe Thr Tyr Ala Pro Pro Lys Leu Arg Ser Glu Met Ile 195 200 205	1090
gcc aga gtg gcc atg cac tgc ctg tgg cat ggc acg ccc aag gac agg Glu Ala Ile Arg Glu Ala Val Val Tyr Leu Ala His Thr His Asp Gly 210 215 220	1138
aaa gtg att gtg aaa aca atg aag act tat gtt gaa aag gtg gct aat Ala Arg Val Ala Met His Cys Leu Trp His Gly Thr Pro Lys Asp Arg 225 230 235 240	1186
ggc caa tac tcc cat ttg gtt tta ctg gcg gca ttt gat tgt att gat Lys Val Ile Val Lys Thr Met Lys Thr Val Glu Lys Val Ala Asn 245 250 255	1234
gat act aag ctt gtg aag cag ata atc ata tca gaa att atc agt tca Gly Gln Tyr Ser His Leu Val Leu Ala Ala Phe Asp Cys Ile Asp 260 265 270	1282
ttg cct agc ata gta aat gac aaa tat gga agg aag gtc cta ttg tac Asp Thr Lys Leu Val Lys Gln Ile Ile Ser Glu Ile Ile Ser Ser 275 280 285	1330
tta cta agc ccc aga gat cct gca cat aca gta cga gaa atc att gaa Leu Pro Ser Ile Val Asn Asp Lys Tyr Gly Arg Lys Val Leu Leu Tyr 290 295 300	1378
gtt ctg caa aaa gga gat gga aat gca cac agt aag aaa gat aca gag Leu Leu Ser Pro Arg Asp Pro Ala His Thr Val Arg Glu Ile Ile Glu 305 310 315 320	1426
gtc cgc aga cgg gag ctc cta gaa tcc att tct cca gct ttg tta agc Val Leu Gln Lys Gly Asp Gly Asn Ala His Ser Lys Lys Asp Thr Glu 325 330 335	1474
tac ctg caa gaa cac gcc caa gaa gtg gtg cta gat aag tct gcg tgt Val Arg Arg Glu Leu Leu Glu Ser Ile Ser Pro Ala Leu Leu Ser 340 345 350	1522
gtg ttg gtg tct gac att ctg gga tct gcc act gga gac gtt cag cct Tyr Leu Gln Glu His Ala Gln Glu Val Val Leu Asp Lys Ser Ala Cys 355 360 365	1570
acc atg aat gcc atc gcc agc ttg gca gca aca gga ctg cat cct ggt Val Leu Val Ser Asp Ile Leu Gly Ser Ala Thr Gly Asp Val Gln Pro 370 375 380	1618
ggc aag gac gga gag ctt cac att gca gaa cat cct gca gga cat cta Thr Met Asn Ala Ile Ala Ser Leu Ala Ala Thr Gly Leu His Pro Gly	1666

385	390	395	400	
gtt ctg aag tgg tta ata gag caa gat aaa aag atg aaa gaa aat ggg Gly Lys Asp Gly Glu Leu His Ile Ala Glu His Pro Ala Gly His Leu 405 410 415				1714
aga gaa ggt tgt ttt gca aaa aca ctt gta gag cat gtt ggt atg aag Val Leu Lys Trp Leu Ile Glu Gln Asp Lys Lys Met Lys Glu Asn Gly 420 425 430				1762
aac ctg aag tcc tgg gct agt gta aat cga ggt gcc att att ctt tct Arg Glu Gly Cys Phe Ala Lys Thr Leu Val Glu His Val Gly Met Lys 435 440 445				1810
agc ctc ctc cag agt tgt gac ctg gaa gtt gca aac aaa gtc aaa gct Asn Leu Lys Ser Trp Ala Ser Val Asn Arg Gly Ala Ile Ile Leu Ser 450 455 460				1858
gca ctg aaa agc ttg att cct aca ctg gaa aaa acc aaa agc acc agc Ser Leu Leu Gln Ser Cys Asp Leu Glu Val Ala Asn Lys Val Lys Ala 465 470 475 480				1906
aaa gga ata gaa att cta ctt gaa aaa ctg agc aca taggtggaaa Ala Leu Lys Ser Leu Ile Pro Thr Leu Glu Lys Thr Lys Ser Thr Ser 485 490 495				1952
gagtttaagag caagatgaa tgatttttc tgttctctgt tctgtttccc aatgcagaaa Lys Gly Ile Glu Ile Leu Leu Glu Lys Leu Ser Thr 500 505				2012
agaagggtta gggtccacca tactggtaat tgggtactc tgtatatgtg ttttttttt gtatacgaat ctatttatat aaattgtttt tttaaatgg 2112				2072
<210> 10				
<211> 508				
<212> PRT				
<213> Homo sapiens				
<400> 10				
Met Trp Glu Ile Leu Arg Arg Lys Asp Cys Asp Lys Glu Lys Arg Val 1 5 10 15				
Lys Leu Met Ser Asp Leu Gln Lys Leu Ile Gln Gly Lys Ile Lys Thr 20 25 30				
Ile Ala Phe Ala His Asp Ser Thr Arg Val Ile Gln Cys Tyr Ile Gln 35 40 45				
Tyr Gly Asn Glu Glu Gln Arg Lys Gln Ala Phe Glu Leu Arg Asp 50 55 60				
Asp Leu Val Glu Leu Ser Lys Ala Lys Tyr Ser Arg Asn Ile Val Lys 65 70 75 80				
Lys Phe Leu Met Tyr Gly Ser Lys Pro Gln Ile Ala Glu Ile Ile Arg 85 90 95				
Ser Phe Lys Gly His Val Arg Lys Met Leu Arg His Ala Glu Ala Ser 100 105 110				
Ala Ile Val Glu Tyr Ala Tyr Asn Asp Lys Ala Ile Leu Glu Gln Arg 115 120 125				
Asn Met Leu Thr Glu Glu Leu Tyr Gly Asn Thr Phe Gln Leu Tyr Lys 130 135 140				
Ser Ala Asp His Arg Thr Leu Asp Lys Val Leu Glu Val Gln Pro Glu 145 150 155 160				

Lys Leu Glu Leu Ile Met Asp Glu Met Lys Gln Ile Leu Thr Pro Met
 165 170 175
 Ala Gln Lys Glu Ala Val Ile Lys His Ser Leu Val His Lys Val Phe
 180 185 190
 Leu Asp Phe Phe Thr Tyr Ala Pro Pro Lys Leu Arg Ser Glu Met Ile
 195 200 205
 Glu Ala Ile Arg Glu Ala Val Val Tyr Leu Ala His Thr His Asp Gly
 210 215 220
 Ala Arg Val Ala Met His Cys Leu Trp His Gly Thr Pro Lys Asp Arg
 225 230 235 240
 Lys Val Ile Val Lys Thr Met Lys Thr Tyr Val Glu Lys Val Ala Asn
 245 250 255
 Gly Gln Tyr Ser His Leu Val Leu Ala Ala Phe Asp Cys Ile Asp
 260 265 270
 Asp Thr Lys Leu Val Lys Gln Ile Ile Ser Glu Ile Ile Ser Ser
 275 280 285
 Leu Pro Ser Ile Val Asn Asp Lys Tyr Gly Arg Lys Val Leu Leu Tyr
 290 295 300
 Leu Leu Ser Pro Arg Asp Pro Ala His Thr Val Arg Glu Ile Ile Glu
 305 310 315 320
 Val Leu Gln Lys Gly Asp Gly Asn Ala His Ser Lys Lys Asp Thr Glu
 325 330 335
 Val Arg Arg Arg Glu Leu Leu Glu Ser Ile Ser Pro Ala Leu Leu Ser
 340 345 350
 Tyr Leu Gln Glu His Ala Gln Glu Val Val Leu Asp Lys Ser Ala Cys
 355 360 365
 Val Leu Val Ser Asp Ile Leu Gly Ser Ala Thr Gly Asp Val Gln Pro
 370 375 380
 Thr Met Asn Ala Ile Ala Ser Leu Ala Ala Thr Gly Leu His Pro Gly
 385 390 395 400
 Gly Lys Asp Gly Glu Leu His Ile Ala Glu His Pro Ala Gly His Leu
 405 410 415
 Val Leu Lys Trp Leu Ile Glu Gln Asp Lys Lys Met Lys Glu Asn Gly
 420 425 430
 Arg Glu Gly Cys Phe Ala Lys Thr Leu Val Glu His Val Gly Met Lys
 435 440 445
 Asn Leu Lys Ser Trp Ala Ser Val Asn Arg Gly Ala Ile Ile Leu Ser
 450 455 460
 Ser Leu Leu Gln Ser Cys Asp Leu Glu Val Ala Asn Lys Val Lys Ala
 465 470 475 480
 Ala Leu Lys Ser Leu Ile Pro Thr Leu Glu Lys Thr Lys Ser Thr Ser
 485 490 495
 Lys Gly Ile Glu Ile Leu Leu Glu Lys Leu Ser Thr
 500 505

<210> 11
 <211> 2457
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>
 <221> CDS
 <222> (645)...(1655)
 <223> NCA3

<400> 11
 ggatccctct gtgaggccga ttatgcaggc ctagaccgc acgtgaccac ttcgagagca 60
 agttgcctgc gagttctct gcccggagaa aaagaaaatgg aggcaattta cttaatatgg 120

tatgagagga tctttgacg gcaaatagat gcgccatctc cgagaaaaaa tctagacaat 180
 aacagcgaca attaacctaa agaggataga agatcgagca aaaaaatttt ttaatatggg 240
 gtcagtggcg atattatact ataggagtt aagagtaagt tgagtgtaaag gtggtagaat 300
 tatgattgaa ctccgaaact aagcgccgat tatgggtggc aaagcggaca gctttgata 360
 tataatcgat cgctctcgta gttgatatcc tctcttgc ttatctttc ctgtatata 420
 tataatgtgtata catacagata cgaatatacc tcagtttagtt tggttaaca ttaaatattc 480
 aacagttgcc agtagaaaaa agaatatacc cattcatttc gagcttttc gtctcattac 540
 tgatatccaa ctaacagtct cctcatagac ggtaccttac tttcttaaa tattaaaata 600
 cttagatatact cgcacataact taactcgctc ctctctaaca cata atg aaa att tcc 656
 Met Lys Ile Ser
 1

gca gct tta ata ttg tct tcc ctt tct gtc gca ttt tct gcc cct 704
 Ala Ala Leu Ile Leu Ser Ser Leu Ser Ser Val Ala Phe Ser Ala Pro
 5 10 15 20

gca cct gct cca gcg gac agt cat cat gaa gat cat cac aaa gat gaa 752
 Ala Pro Ala Pro Ala Asp Ser His His Glu Asp His His Lys Asp Glu
 25 30 35

aaa cca gcg gtt gtc act gtc act caa tac ata gat tcc aat gcc gct 800
 Lys Pro Ala Val Val Thr Val Thr Gln Tyr Ile Asp Ser Asn Ala Ala
 40 45 50

act agt act gta gaa tct gct gct act acc act aca ttg tcc tca tct 848
 Thr Ser Thr Val Glu Ser Ala Ala Thr Thr Thr Leu Ser Ser Ser
 55 60 65

gag aag gat acc tct gaa cag aag cgt gat ggc gga ttc caa gat ggt 896
 Glu Lys Asp Thr Ser Glu Gln Lys Arg Asp Gly Gly Phe Gln Asp Gly
 70 75 80

act gtc aaa tgt tcg gac ttc cct tct gta aac ggt ata gtt tcc ttg 944
 Thr Val Lys Cys Ser Asp Phe Pro Ser Val Asn Gly Ile Val Ser Leu
 85 90 95 100

gac tgg cta gga ttt ggt gga tgg gcc tct gtc atg gac atg gat gcc 992
 Asp Trp Leu Gly Phe Gly Trp Ala Ser Val Met Asp Met Asp Ala
 105 110 115

aac act tcg tcc gaa tgt aag gat ggc tac tac tgt tct tat gca tgt 1040
 Asn Thr Ser Glu Cys Lys Asp Gly Tyr Tyr Cys Ser Tyr Ala Cys
 120 125 130

gaa cct gga atg tca aag act caa tgg cct tct gac caa cca agc gat 1088
 Glu Pro Gly Met Ser Lys Thr Gln Trp Pro Ser Asp Gln Pro Ser Asp
 135 140 145

ggt aaa tct gtt ggt ggt ctt tat tgt aaa aat ggt tac ttg tac cgt 1136
 Gly Lys Ser Val Gly Gly Leu Tyr Cys Lys Asn Gly Tyr Leu Tyr Arg
 150 155 160

acc aac act gat acc agc gat tta tgt tct acg gat gaa aca tct gct 1184
 Thr Asn Thr Asp Thr Ser Asp Leu Cys Ser Thr Asp Glu Thr Ser Ala
 165 170 175 180

aag gcc att aac aaa aag tct gac tcc att gct cta tgt agg acg gat 1232
 Lys Ala Ile Asn Lys Lys Ser Asp Ser Ile Ala Leu Cys Arg Thr Asp
 185 190 195

tac cca gga tct gaa aac atg gtg att ccc aca gtg gtt gat ggt gga Tyr Pro Gly Ser Glu Asn Met Val Ile Pro Thr Val Val Asp Gly Gly 200 205 210	1280
gat tca caa cca att tca gtc gtt gat gaa gac act tat tat caa tgg Asp Ser Gln Pro Ile Ser Val Val Asp Glu Asp Thr Tyr Tyr Gln Trp 215 220 225	1328
cag ggt aaa aag act tct gct cag tac tat att aac aac gcc ggt gta Gln Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Ile Asn Asn Ala Gly Val 230 235 240	1376
tct gca gaa gat ggg tgc att tgg ggt act tct ggt tcg gat gtc ggc Ser Ala Glu Asp Gly Cys Ile Trp Gly Thr Ser Gly Ser Asp Val Gly 245 250 255 260	1424
aac tgg gct cca cta gtg tta ggt gct tcc act aat gga gaa aca Asn Trp Ala Pro Leu Val Leu Gly Ala Gly Ser Thr Asn Gly Glu Thr 265 270 275	1472
tac ttg tcg ttg att cca aac ccc aac agt aac caa gct gcc aac ttt Tyr Leu Ser Leu Ile Pro Asn Pro Asn Ser Asn Gln Ala Ala Asn Phe 280 285 290	1520
aac gtt aaa ata gtt gca tcc gat ggc gct aac gtt cag ggc agc tgt Asn Val Lys Ile Val Ala Ser Asp Gly Ala Asn Val Gln Gly Ser Cys 295 300 305	1568
gcg tat gaa gat ggc tct ttc acc gga gat ggt tcc gat ggt tgc aca Ala Tyr Glu Asp Gly Ser Phe Thr Gly Asp Gly Ser Asp Gly Cys Thr 310 315 320	1616
gtt tct gtt tta tct gga tct gct gaa ttt gtt ttc tat taagtcactc Val Ser Val Leu Ser Gly Ser Ala Glu Phe Val Phe Tyr 325 330 335	1665
ttctttcgg taaaagaatg tcttgattt tgataccctc aattccccttt attattctttt ttctccgct ctctatttat tattatacat tgggattccg ttatattttt ctcccttcag ttcattttac ttctaaaaaa gtttcgttga tcgctattat gctatggatt caaagatttt ctttctctc tcttcaaggt gtactctgca ttacggtttt cttagttcg tttatttttt tttgttaac aagggtttt gatacatata tataaatata tgaaaatatt atagtgtta tttgttact tcctgcgagt tgcaacagaa ctaacaagat gccatgctgt tttttttcat ttttggcta taaaataaac agtatacctag tccttggtt cggtttaaa atggaaattgc aaaccctata attccttcct cacaccgaac aaaccgccta gtagtcgatt ttcagagact ctaatgcttt gaatataatt tttttctca aaaatttcct taagcgtgct atcgaatgag tagacatcaa tcaagagttt catggctcc ccgtatttgc cgctgcttct aatattttt gagtgtagca tagcccaatc aatcaaattc tcgataatgc cacttttac atatacacga cgacaaccca cagtagtaac actcatgact aaatttcat cagacttaa tgtcatgtta ggggctaacg aaatcaatgc aatgggcgtt tctctataaa cgatgatatg cgtattgttc accactggat cc	1725 1785 1845 1905 1965 2025 2085 2145 2205 2265 2325 2385 2445 2457

<210> 12
<211> 337
<212> PRT
<213> Saccharomyces cerevisiae

<400> 12
Met Lys Ile Ser Ala Ala Leu Ile Leu Ser Ser Leu Ser Ser Val Ala

1	5	10	15												
Phe	Ser	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Asp	Ser	His	His	Glu	Asp	His
20									25						30
His	Lys	Asp	Glu	Lys	Pro	Ala	Val	Val	Thr	Val	Thr	Gln	Tyr	Ile	Asp
35									40						45
Ser	Asn	Ala	Ala	Thr	Ser	Thr	Val	Glu	Ser	Ala	Ala	Thr	Thr	Thr	Thr
50									55						60
Leu	Ser	Ser	Ser	Glu	Lys	Asp	Thr	Ser	Glu	Gln	Lys	Arg	Asp	Gly	Gly
65									70						80
Phe	Gln	Asp	Gly	Thr	Val	Lys	Cys	Ser	Asp	Phe	Pro	Ser	Val	Asn	Gly
									85						95
Ile	Val	Ser	Leu	Asp	Trp	Leu	Gly	Phe	Gly	Gly	Trp	Ala	Ser	Val	Met
									100						110
Asp	Met	Asp	Ala	Asn	Thr	Ser	Ser	Glu	Cys	Lys	Asp	Gly	Tyr	Tyr	Cys
									115						125
Ser	Tyr	Ala	Cys	Glu	Pro	Gly	Met	Ser	Lys	Thr	Gln	Trp	Pro	Ser	Asp
									130						140
Gln	Pro	Ser	Asp	Gly	Lys	Ser	Val	Gly	Gly	Leu	Tyr	Cys	Lys	Asn	Gly
									145						160
Tyr	Leu	Tyr	Arg	Thr	Asn	Thr	Asp	Thr	Ser	Asp	Leu	Cys	Ser	Thr	Asp
									165						175
Glu	Thr	Ser	Ala	Lys	Ala	Ile	Asn	Lys	Ser	Asp	Ser	Ile	Ala	Leu	
									180						190
Cys	Arg	Thr	Asp	Tyr	Pro	Gly	Ser	Glu	Asn	Met	Val	Ile	Pro	Thr	Val
									195						205
Val	Asp	Gly	Gly	Asp	Ser	Gln	Pro	Ile	Ser	Val	Val	Asp	Glu	Asp	Thr
									210						220
Tyr	Tyr	Gln	Trp	Gln	Gly	Lys	Lys	Thr	Ser	Ala	Gln	Tyr	Tyr	Ile	Asn
									225						240
Asn	Ala	Gly	Val	Ser	Ala	Glu	Asp	Gly	Cys	Ile	Trp	Gly	Thr	Ser	Gly
									245						255
Ser	Asp	Val	Gly	Asn	Trp	Ala	Pro	Leu	Val	Leu	Gly	Ala	Gly	Ser	Thr
									260						270
Asn	Gly	Glu	Thr	Tyr	Leu	Ser	Leu	Ile	Pro	Asn	Pro	Asn	Ser	Asn	Gln
									275						285
Ala	Ala	Asn	Phe	Asn	Val	Lys	Ile	Val	Ala	Ser	Asp	Gly	Ala	Asn	Val
									290						300
Gln	Gly	Ser	Cys	Ala	Tyr	Glu	Asp	Gly	Ser	Phe	Thr	Gly	Asp	Gly	Ser
									305						320
Asp	Gly	Cys	Thr	Val	Ser	Val	Leu	Ser	Gly	Ser	Ala	Glu	Phe	Val	Phe
									325						335
Tyr															

<210> 13
<211> 2150
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (563)...(1987)
<223> SAG1

<400> 13
tgtttagtgc taccccaacta cttacattcc tttaaaaacc acaatattta agttaacctg 60
agctttattt ttagtaagtt atttaccaca atttttctca tacaccttta caatccgtat 120
tgccatgaat accaaggcgtt gctcagcttc tgccagcgtt caacccttcc caataccggcc 180

aatgcgtcct caaaacgtta gtttagtcgt gctcaaccgc tattttggc tttatccg 240			
tttcttcctc ctgaacgaca ttgcgtcacga aaattgcggc gaaaaatttc ctgatgcgga 300			
cacttttcc cgatccggac atgcctttt ttggcggttgc gctcagtc atagaagttt 360			
cagatctaca ttaggaagaa ccagaaaata gccatcatg ctttcagcat agcacagcat 420			
agcagctgtg tataatctaa ataagatgtt gactgggttgc catttgaaa gggtttgtgt 480			
aagaaaagca atacttgagg taaaacaaga gaaaaaaaaa cactttacta actaatatcc 540			
aatcctttat tttttgcag aa atg aaa ttc tca act gcc gtt act acg ttg 592			
Met Lys Phe Ser Thr Ala Val Thr Thr Leu			
1 5 10			
att agt tct ggt gcc atc gtg tct gct tta cca cac gtg gat gtt cac 640			
Ile Ser Ser Gly Ala Ile Val Ser Ala Leu Pro His Val Asp Val His			
15 20 25			
caa gaa gat gcc cac caa cat aag agg gcc gtt gcg tac aaa tac gtt 688			
Gln Glu Asp Ala His Gln His Lys Arg Ala Val Ala Tyr Lys Tyr Val			
30 35 40			
tac gaa act gtt gtt gtc gat tct gat ggc cac act gta act cct gct 736			
Tyr Glu Thr Val Val Asp Ser Asp Gly His Thr Val Thr Pro Ala			
45 50 55			
gct tca gaa gtc gct act gct gct acc tct gct atc att aca aca tct 784			
Ala Ser Glu Val Ala Thr Ala Ala Thr Ser Ala Ile Ile Thr Thr Ser			
60 65 70			
gtg ttg gct cca acc tcc tcc gca gcc gct ggg ata gcc gct tcc att 832			
Val Leu Ala Pro Thr Ser Ser Ala Ala Ala Gly Ile Ala Ala Ser Ile			
75 80 85 90			
gct gtt tca tct gct gcc tta gcc aag aat gag aaa atc tct gat gcc 880			
Ala Val Ser Ser Ala Ala Leu Ala Lys Asn Glu Lys Ile Ser Asp Ala			
95 100 105			
gct gca tct gcc act gcc tca aca tct caa ggg gca tcc tcc tcc 928			
Ala Ala Ser Ala Thr Ala Ser Thr Ser Gln Gly Ala Ser Ser Ser Ser			
110 115 120			
tcc tcc tcc tcg gca act tct acc cta gaa agc agc tct gtt tct tca 976			
Ser Ser Ser Ala Thr Ser Thr Leu Glu Ser Ser Ser Val Ser Ser			
125 130 135			
tct agt gaa gaa gct gct cca aca tct act gtc gtg tca act tct tcc 1024			
Ser Ser Glu Glu Ala Ala Pro Thr Ser Thr Val Val Ser Thr Ser Ser			
140 145 150			
gca acc caa tct agt gct tct tct gcc act aaa tct agt act tct tcc 1072			
Ala Thr Gln Ser Ser Ala Ser Ser Ala Thr Lys Ser Ser Thr Ser Ser			
155 160 165 170			
act tca cca tct act tct act tcc act tct tct act tcc tct 1120			
Thr Ser Pro Ser Thr Ser Thr Ser Thr Ser Ser Thr Ser Ser Ser			
175 180 185			
tcc tct tcc tcc tcc tcc tct tct tct tct tct ggc agt ggt 1168			
Ser Gly Ser Gly			
190 195 200			
agt atc tac ggt gat ttg gcc gac ttt tca ggc cca agt gag aaa ttc 1216			

Ser Ile Tyr Gly Asp Leu Ala Asp Phe Ser Gly Pro Ser Glu Lys Phe			
205	210	215	
caa gac ggc act att cca tgt gac aaa ttc cca tct ggt caa ggt gtc			1264
Gln Asp Gly Thr Ile Pro Cys Asp Lys Phe Pro Ser Gly Gln Gly Val			
220	225	230	
att tct att gac tgg att ggc gag ggt gga tgg tcc ggt gtg gaa aac			1312
Ile Ser Ile Asp Trp Ile Gly Glu Gly Gly Trp Ser Gly Val Glu Asn			
235	240	245	250
acc gac act tcc act ggc ggt tca tgc aag gag ggg tcc tac tgt tcc			1360
Thr Asp Thr Ser Thr Gly Gly Ser Cys Lys Glu Gly Ser Tyr Cys Ser			
255	260	265	
tac tcc tgc caa cca ggt atg tct aag acc caa tgg cca tcc gat caa			1408
Tyr Ser Cys Gln Pro Gly Met Ser Lys Thr Gln Trp Pro Ser Asp Gln			
270	275	280	
cca tct gac ggt aga tct gtc ggg ggt ttg ttg tgt aaa aat ggt tat			1456
Pro Ser Asp Gly Arg Ser Val Gly Gly Leu Leu Cys Lys Asn Gly Tyr			
285	290	295	
ttg tac cgt tct aac act gac gcg gat tac tta tgt gaa tgg ggt gtc			1504
Leu Tyr Arg Ser Asn Thr Asp Ala Asp Tyr Leu Cys Glu Trp Gly Val			
300	305	310	
gag gct gcc tat gtt gtt tct aaa cta agc aag ggt gtc gcc att tgc			1552
Glu Ala Ala Tyr Val Val Ser Lys Leu Ser Lys Gly Val Ala Ile Cys			
315	320	325	330
aga acc gac tac ccg ggc act gaa aac atg gtt atc cca acc tat gtt			1600
Arg Thr Asp Tyr Pro Gly Thr Glu Asn Met Val Ile Pro Thr Tyr Val			
335	340	345	
gaa ggg ggt agc tct ttg cca ttg acc gtt gtt gac caa gat act tac			1648
Glu Gly Gly Ser Ser Leu Pro Leu Thr Val Val Asp Gln Asp Thr Tyr			
350	355	360	
ttt act tgg gaa ggc aaa aag aca tct gct caa tac tac gtt aat aac			1696
Phe Thr Trp Glu Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Val Asn Asn			
365	370	375	
gcc ggc gtc tca gtt gaa gat ggg tgt atc tgg ggt act tct gga tct			1744
Ala Gly Val Ser Val Glu Asp Gly Cys Ile Trp Gly Thr Ser Gly Ser			
380	385	390	
ggt att ggt aac tgg gca cca tta aac ttt ggt gct ggc tcc act ggt			1792
Gly Ile Gly Asn Trp Ala Pro Leu Asn Phe Gly Ala Gly Ser Thr Gly			
395	400	405	410
gga gtg aca tac tta tca ttg att cct aac cca aac aac agc gac gca			1840
Gly Val Thr Tyr Leu Ser Leu Ile Pro Asn Pro Asn Asn Ser Asp Ala			
415	420	425	
ttg aac tac aac gtc aag ata gtt gct gct gat gat tca tcc aat gtc			1888
Leu Asn Tyr Asn Val Lys Ile Val Ala Ala Asp Asp Ser Ser Asn Val			
430	435	440	

atc ggt gaa tgt gtt tac gaa aat ggt gag ttc tct ggc ggt gct gac Ile Gly Cys Val Tyr Glu Asn Gly Glu Phe Ser Gly Gly Ala Asp 445 450 455	1936
ggg tgt acc gtc tct gtt act tcc ggt aaa gct cat ttc gtc tta tac Gly Cys Thr Val Ser Val Thr Ser Gly Lys Ala His Phe Val Leu Tyr 460 465 470	1984
aat taagctacgt gactactact tttcctttt tttttctttt ttcaacaca Asn 475	2037
tctcacccccc tatacctcac acaatcacta tggcccctt ttcttttac cgatatttat actgtccacc ttttctttt cgttaatggc ctcaatgttt ctgtaccatt atc	2097 2150
<210> 14	
<211> 475	
<212> PRT	
<213> <i>Saccharomyces cerevisiae</i>	
<400> 14	
Met Lys Phe Ser Thr Ala Val Thr Thr Leu Ile Ser Ser Gly Ala Ile 1 5 10 15	
Val Ser Ala Leu Pro His Val Asp Val His Gln Glu Asp Ala His Gln 20 25 30	
His Lys Arg Ala Val Ala Tyr Lys Tyr Val Tyr Glu Thr Val Val Val 35 40 45	
Asp Ser Asp Gly His Thr Val Thr Pro Ala Ala Ser Glu Val Ala Thr 50 55 60	
Ala Ala Thr Ser Ala Ile Ile Thr Thr Ser Val Leu Ala Pro Thr Ser 65 70 75 80	
Ser Ala Ala Ala Gly Ile Ala Ala Ser Ile Ala Val Ser Ser Ala Ala 85 90 95	
Leu Ala Lys Asn Glu Lys Ile Ser Asp Ala Ala Ala Ser Ala Thr Ala 100 105 110	
Ser Thr Ser Gln Gly Ala Ser Ser Ser Ser Ser Ser Ala Thr 115 120 125	
Ser Thr Leu Glu Ser Ser Ser Val Ser Ser Ser Ser Glu Glu Ala Ala 130 135 140	
Pro Thr Ser Thr Val Val Ser Thr Ser Ser Ala Thr Gln Ser Ser Ala 145 150 155 160	
Ser Ser Ala Thr Lys Ser Ser Thr Ser Ser Thr Ser Pro Ser Thr Ser 165 170 175	
Thr Ser Thr Ser Thr Ser Ser 180 185 190	
Ser Ser Ser Ser Ser Ser Gly Ser Gly Ser Ile Tyr Gly Asp Leu 195 200 205	
Ala Asp Phe Ser Gly Pro Ser Glu Lys Phe Gln Asp Gly Thr Ile Pro 210 215 220	
Cys Asp Lys Phe Pro Ser Gly Gln Gly Val Ile Ser Ile Asp Trp Ile 225 230 235 240	
Gly Glu Gly Gly Trp Ser Gly Val Glu Asn Thr Asp Thr Ser Thr Gly 245 250 255	
Gly Ser Cys Lys Glu Gly Ser Tyr Cys Ser Tyr Ser Cys Gln Pro Gly 260 265 270	
Met Ser Lys Thr Gln Trp Pro Ser Asp Gln Pro Ser Asp Gly Arg Ser 275 280 285	
Val Gly Gly Leu Leu Cys Lys Asn Gly Tyr Leu Tyr Arg Ser Asn Thr 290 295 300	

Asp Ala Asp Tyr Leu Cys Glu Trp Gly Val Glu Ala Ala Tyr Val Val
 305 310 315 320
 Ser Lys Leu Ser Lys Gly Val Ala Ile Cys Arg Thr Asp Tyr Pro Gly
 325 330 335
 Thr Glu Asn Met Val Ile Pro Thr Tyr Val Glu Gly Gly Ser Ser Leu
 340 345 350
 Pro Leu Thr Val Val Asp Gln Asp Thr Tyr Phe Thr Trp Glu Gly Lys
 355 360 365
 Lys Thr Ser Ala Gln Tyr Tyr Val Asn Asn Ala Gly Val Ser Val Glu
 370 375 380
 Asp Gly Cys Ile Trp Gly Thr Ser Gly Ser Gly Ile Gly Asn Trp Ala
 385 390 395 400
 Pro Leu Asn Phe Gly Ala Gly Ser Thr Gly Gly Val Thr Tyr Leu Ser
 405 410 415
 Leu Ile Pro Asn Pro Asn Asn Ser Asp Ala Leu Asn Tyr Asn Val Lys
 420 425 430
 Ile Val Ala Ala Asp Asp Ser Ser Asn Val Ile Gly Glu Cys Val Tyr
 435 440 445
 Glu Asn Gly Glu Phe Ser Gly Gly Ala Asp Gly Cys Thr Val Ser Val
 450 455 460
 Thr Ser Gly Lys Ala His Phe Val Leu Tyr Asn
 465 470 475

<210> 15
 <211> 145
 <212> PRT
 <213> Saccharomyces cerevisiae

<220>
 <221> VARIANT
 <222> (1)...(145)
 <223> Xaa = Any Amino Acid

<400> 15
 Thr Asp Tyr Pro Gly Xaa Glu Asn Met Val Xaa Pro Thr Xaa Val Xaa
 1 5 10 15
 Xaa Gly Xaa Ser Xaa Pro Xaa Xaa Val Xaa Xaa Xaa Asp Xaa Tyr Xaa
 20 25 30
 Xaa Trp Xaa Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Xaa Asn Asn Xaa
 35 40 45
 Gly Val Ser Xaa Glu Asp Gly Cys Ile Trp Gly Thr Xaa Gly Ser Xaa
 50 55 60
 Xaa Gly Asn Trp Ala Pro Xaa Xaa Xaa Gly Ala Xaa Xaa Xaa Thr Xaa Gly
 65 70 75 80
 Xaa Thr Tyr Leu Ser Xaa Ile Pro Asn Pro Asn Xaa Xaa Xaa Ala Xaa
 85 90 95
 Asn Xaa Asn Xaa Lys Ile Val Ala Xaa Asp Xaa Xaa Xaa Val Xaa
 100 105 110
 Gly Xaa Cys Xaa Tyr Glu Xaa Gly Xaa Xaa Xaa Gly Xaa Gly Xaa Asp
 115 120 125
 Gly Cys Thr Val Ser Val Xaa Ser Gly Xaa Ala Xaa Phe Val Xaa Tyr
 130 135 140
 Xaa
 145

<210> 16
 <211> 60

<212> PRT

<213> Saccharomyces cerevisiae

<400> 16

Ser Leu Ile Pro Asn Pro Asn Asn Gly Asn Ala Leu Asn Phe Asn Val
1 5 10 15
Lys Ile Val Ala Ala Asp Asp Ser Ser Thr Val Asn Gly Glu Cys Ile
20 25 30
Tyr Glu Asn Gly Ser Phe Ser Ser Gly Gly Ser Asp Gly Cys Thr Val
35 40 45
Ser Val Thr Ala Gly Lys Ala Lys Phe Val Leu Tyr
50 55 60

<210> 17

<211> 16

<212> PRT

<213> Saccharomyces cerevisiae

<400> 17

Leu Ala Thr Asp Gln Phe Gly Cys Arg Phe Leu Gln Lys Lys Leu Glu
1 5 10 15

<210> 18

<211> 16

<212> PRT

<213> Saccharomyces cerevisiae

<400> 18

Leu Ile Leu Asp Pro Phe Gly Asn Tyr Leu Val Asp Lys Ile Cys Asp
1 5 10 15

<210> 19

<211> 16

<212> PRT

<213> Saccharomyces cerevisiae

<400> 19

Ile Ser Ile Asn Gln Tyr Gly Thr Arg Ser Leu Gln Lys Ile Ile Asp
1 5 10 15

<210> 20

<211> 15

<212> PRT

<213> Saccharomyces cerevisiae

<400> 20

Leu Ile Asn Asp Ile Asn Gly His Val Ile Gln Lys Cys Ile Phe
1 5 10 15

<210> 21

<211> 16

<212> PRT

<213> Saccharomyces cerevisiae

<400> 21
Ile Ser Thr His Lys His Gly Cys Cys Val Leu Gln Lys Ile Leu Ser
1 5 10 15

<210> 22
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 22
Leu Ile Asn Asp Gln Phe Gly Asn Tyr Ile Ile Gln Phe Ile Leu Asp
1 5 10 15

<210> 23
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 23
Leu Ser Cys Leu Lys Phe Ser Ser Asn Val Val Glu Lys Phe Ile Lys
1 5 10 15

<210> 24
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 24
Leu Ile Arg Asp Asn Phe Gly Asn Tyr Ala Leu Gln Thr Leu Leu Asp
1 5 10 15

<210> 25
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 25
Leu Cys Lys Asp Gln His Gly Cys Arg Phe Leu Gln Lys Gln Leu Asp
1 5 10 15

<210> 26
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 26
Leu Met Thr Asp Ser Phe Gly Asn Tyr Leu Ile Gln Lys Leu Leu Glu
1 5 10 15

<210> 27
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 27
Ile Ser Leu Asn Pro His Gly Thr Arg Ala Leu Gln Lys Leu Ile Glu
1 5 10 15

<210> 28
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 28
Leu Ser Lys Asp Leu Asn Gly Asn His Val Ile Gln Lys Cys Leu Gln
1 5 10 15

<210> 29
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 29
Ile Ala Thr His Arg His Gly Cys Cys Val Leu Gln Arg Cys Leu Asp
1 5 10 15

<210> 30
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 30
Leu Thr Leu Asp Pro Phe Gly Asn Tyr Val Val Gln Tyr Ile Ile Thr
1 5 10 15

<210> 31
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 31
Leu Ser Ile His Lys Phe Gly Ser Asn Val Ile Glu Lys Ile Ile Lys
1 5 10 15

<210> 32
<211> 16
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 32
Leu Leu Asn Asp Ser Tyr Gly Asn Tyr Val Leu Gln Thr Ala Leu Asp
1 5 10 15

<210> 33
<211> 16
<212> PRT
<213> *Drosophila*

<400> 33
Phe Ser Gln Asp Gln His Gly Ser Arg Phe Ile Gln Gln Lys Leu Glu
1 5 10 15

<210> 34
<211> 16
<212> PRT
<213> Drosophila

<400> 34
Leu Met Thr Asp Val Phe Gly Asn Tyr Val Ile Gln Lys Phe Phe Glu
1 5 10 15

<210> 35
<211> 16
<212> PRT
<213> Drosophila

<400> 35
Leu Ala Leu Gln Met Tyr Gly Leu Arg Val Ile Gln Lys Ala Leu Glu
1 5 10 15

<210> 36
<211> 16
<212> PRT
<213> Drosophila

<400> 36
Cys Val Lys Asp Gln Asn Gly Asn His Val Val Gln Lys Cys Ile Glu
1 5 10 15

<210> 37
<211> 16
<212> PRT
<213> Drosophila

<400> 37
Leu Ser Thr His Pro Tyr Gly Cys Arg Val Ile Gln Arg Ile Leu Glu
1 5 10 15

<210> 38
<211> 16
<212> PRT
<213> Drosophila

<400> 38
Leu Ile Gln Asp Gln Tyr Gly Asn Tyr Val Ile Gln His Val Leu Glu
1 5 10 15

<210> 39
<211> 16
<212> PRT
<213> Drosophila

<400> 39
Leu Ser Gln His Lys Phe Ala Ser Asn Val Val Glu Lys Cys Val Thr
1 5 10 15

<210> 40
<211> 16
<212> PRT
<213> Drosophila

<400> 40
Met Met Lys Asp Gln Tyr Ala Asn Tyr Val Val Gln Lys Met Ile Asp
1 5 10 15

<210> 41
<211> 16
<212> PRT
<213> Homo sapiens

<400> 41
Phe Ser Gln Asp Gln His Gly Ser Arg Phe Ile Gln Leu Lys Leu Glu
1 5 10 15

<210> 42
<211> 16
<212> PRT
<213> Homo sapiens

<400> 42
Leu Met Arg Asp Val Phe Gly Asn Tyr Val Ile Gln Lys Phe Phe Glu
1 5 10 15

<210> 43
<211> 16
<212> PRT
<213> Homo sapiens

<400> 43
Leu Ala Leu Gln Met Tyr Gly Leu Arg Val Ile Gln Lys Ala Leu Glu
1 5 10 15

<210> 44
<211> 16
<212> PRT
<213> Homo sapiens

<400> 44
Cys Val Lys Asp Gln Asn Gly Asn His Val Val Gln Lys Cys Ile Glu
1 5 10 15

<210> 45
<211> 16
<212> PRT
<213> Homo sapiens

<400> 45
Leu Ser Thr His Pro Tyr Gly Cys Arg Val Ile Gln Arg Ile Leu Glu
1 5 10 15

<210> 46
<211> 16
<212> PRT
<213> Homo sapiens

<400> 46
Leu Val Gln Asp Gln Tyr Gly Asn Tyr Val Ile Gln His Val Leu Glu
1 5 10 15

<210> 47
<211> 16
<212> PRT
<213> Homo sapiens

<400> 47
Val Leu Ser Gln His Phe Ala Ser Asn Val Val Glu Lys Cys Val Thr
1 5 10 15

<210> 48
<211> 16
<212> PRT
<213> Homo sapiens

<400> 48
Met Met Lys Asp Gln Tyr Ala Asn Tyr Val Val Gln Lys Met Ile Asp
1 5 10 15